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(54) **COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF MYLIP/IDOL GENE**

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(52) **U.S. Cl.**

CPC ***A61K 48/005*** (2013.01); ***C12N 15/113*** (2013.01); ***C12N 15/1137*** (2013.01); *C12N 2310/14* (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

The invention relates to double-stranded ribonucleic acid (dsRNA) compositions targeting the Mylip/Idol gene, and methods of using such dsRNA compositions to inhibit expression of Mylip/Idol.

31 Claims, 4 Drawing Sheets

Figure 1. SEQ ID NO. 644 (Human Mylip/Idol mRNA sequence)

```
   1 agttgggctg ctggagtgcg gcgccaccgc ggaggacagg ggcagctggc gggcagcggg
  61 tgagggggtg gcggggacgc gagtggcggc cgcggggccc cggacaaggg tccgcagagc
 121 tgcagccttc gagggccagc cctctccgag tccggggctg ggtcccacca gtgacaaggc
 181 ggcagccccg cgcacaccaa agagaaggcg gctgtggcgg cagcggcagc cccagccatg
 241 ctgtgttatg tgacgaggcc ggacgcggtg ctgatggagg tggaggtgga ggcgaaagcc
 301 aacggcgagg actgcctcaa ccaggtgtgc aggcgactgg gaatcataga agttgactat
 361 tttggactgc agtttacggg tagcaaaggt gaaagtttat ggctaaacct gagaaaccgg
 421 atctcccagc agatggatgg gctagcccct tacaggctta aacttagagt caagttcttc
 481 gtggagcctc atctcatctt acaggagcag actaggcata tctttttctt gcacatcaag
 541 gaggccctct tggcaggcca cctcttgtgt tccccagagc aggcagtgga actcagtgcc
 601 ctcctggccc agaccaagtt tggagactac aaccagaaca ctgccaagta taactatgag
 661 gagctctgtg ccaaggagct ctcctctgcc accttgaaca gcattgttgc aaaacataag
 721 gagttggagg ggaccagcca ggcttcagct gaataccaag ttttgcagat tgtgtcggca
 781 atggaaaact atggcataga atggcattct gtgcgggata gcgaagggca gaaactgctc
 841 attggggttg gacctgaagg aatctcaatt tgtaaagatg actttagccc aattaatagg
 901 atagcttatc ctgtggtgca gatggccacc cagtcaggaa agaatgtata tttgacggtc
 961 accaaggaat ctgggaacag catcgtgctc ttgtttaaaa tgatcagcac cagggcggcc
1021 agcgggctct accgagcgat aacagagacg cacgcattct acaggtgtga cacagtgacc
1081 agcgccgtga tgatgcagta tagccgtgac ttgaagggcc acttggcatc tctgtttctg
1141 aatgaaaaca ttaaccttgg caagaaatat gtctttgata ttaaaagaac atcaaaggag
1201 gtgtatgacc atgccaggag ggctctgtac aatgctggcg ttgtggacct cgtttcaaga
1261 aacaaccaga gcccttcaca ctcgcctctg aagtcctcag aaagcagcat gaactgcagc
1321 agctgcgagg gcctcagctg ccagcagacc cgggtgctgc aggagaagct acgcaagctg
1381 aaggaagcca tgctgtgcat ggtgtgctgc gaggaggaga tcaactccac cttctgtccc
1441 tgtggccaca ctgtgtgctg tgagagctgc gccgcccagc tacagtcatg tcccgtctgc
1501 aggtcgcgtg tggagcatgt ccagcacgtc tatctgccaa cgcacaccag tcttctcaat
1561 ctgactgtaa tctaatctgt tgtgcttttg ttggacttgg catgtttcca tgaactgcac
1621 tattataaac tattaaaatg atagattgtg gagaaagtaa ttattccaac acccatctgc
1681 catgcgatgt taaaaaaaaa aaaaaggaag aaaaataaca cagctactcc tcactgcaaa
1741 aacatatcca tgcgtagaat caacaactcc agtcatggga ccaggaggag ctctgggacg
1801 cagacacatt ccttggatgt tgatttttt tatgatctag taaaggaata ggtaaagtct
1861 ttgatgtcag tgaagtggca acatagccaa aaagttgggt acctttagg aaatgatgtt
1921 gtaagtctcc ttaatgtatc ctgaggtaag tttcctactg gcagcagatt ttgtaagaat
1981 tacttttaag aatttcattc tttttgtatg gtcatggagc tccaaccatt tttaatagga
2041 aagtcttttg taaattgttg tcgttttaat gtcatttctg tctttataac ttgatcaaga
2101 atgattggaa ggcaaacagg tttacaaatc aattctgtga cttttaaaaa gttgacaatg
2161 ttgtcagatt taaaccagtg tggctagtaa aaagcagctc actcaatgtg ggtggctccc
2221 tattccttta cgctcccccc atccctaccc cacaagcctt tcgattataa aatactacca
2281 atcttgttat aagattactg tggagtagtc aagtactccc cgggccttct gagctggtgg
2341 aatattttat ttcagactga aaacagagag cactctcctt gggaagggaa agcggagctt
2401 gctgagtgag agatggagcc tcatggtgta caactgaggg tagttaactc atcacttctc
2461 ccaagcactc gatcccagct tcacccactg gtgttgcttt gcttgaactg ttcaagcctt
2521 ttatagcctt accataagta tttagatatg gtgtcctttt ctgtttttgg gggggagttt
2581 ttgttgtgtt tttttaaagt aagtgcttaa gtattaactt tgggttgtcc cctctgtatg
2641 tttcgaaggg gttttggttc tttttgcttc tgttttctta aacatgtttt ccactcccac
2701 ttgggcattt tggaagctgg tcagctagca ggttttctgg gatgtcggga gacctagatg
2761 accttatcgg gtgcaatact agctaaggta aagctagaaa cctacactgt cactttactg
2821 agatttctga gtatactttt catattgcct taatgtagca gtaatgtgtt tatgcatttg
2881 tttctttgca cagacatttt gtcaaatatt aaaactctac ttttttatgg cacatattag
2941 catataagcc tttattccaa gaggtattta ttttttcact tgtaaaaaaa taatgtttcc
3001 acgtaaagaa ctctgttata tcctagagga ctctgtcttt tatattcggg ataataaaga
3061 ctttaaagca aaaaaaaaaa aaaaaa
```

Figure 2. SEQ ID NO. 645 (Mouse Mylip/Idol mRNA Sequence; isoform 1)

```
   1 agtagggctg tcggagcggc gcggccgtgt agctcccggg aactggctgt cgtgggggtg
  61 gcggggacgc gagtggcggc tgcgtggggt gcagggcggg tggccgcacg gctgcacctt
 121 cctcacggag cccggagtcg acttggagca attgcggtga ggcgacagct ccggcgcaca
 181 cccgagaaga agcggcggtg gcggcggccc cagccatgct gtgctatgtg acgaggccgg
 241 acgcggtgct gatggaggta gaggtggagg caaaagccaa cggcgaggac tgtctcaacc
 301 aggtgtgcag gcgtctaggg atcatcgagg ttgattattt tgggctgcag ttcacgggga
 361 gcaaaggtga gagcttatgg ctgaatctga gaaaccggat ctcccagcag atggatgggc
 421 tggcacctta ccgccttaaa ctgagggtca agttctttgt ggagcctcat ctcatcttac
 481 aggagcagac aaggcatatc tttttcttgc acattaaaga gtccctcttg gcaggccacc
 541 tccagtgttc cccagagcag gccgtggaac tcagtgccct cctggctcag accaaatttg
 601 gagactacaa ccagaacacc gcccaataca gctatgagga cctgtgtgag aaagagctct
 661 ccagctccac tttgaacagc atcgttgcga agcataagga gctggagggc atcagccagg
 721 cctctgccga gtaccaggtt ctgcagattg tgtcagcgat ggagaactac ggcatagagt
 781 ggcatgctgt gagggacagc gaaggacaga aactcctcat tggggtcgga cctgaaggca
 841 tctcgatctg taaagaggac tttagcccta ttaacaggat agcttatcct gtggtgcaga
 901 tggccaccca gtcaggaaag aatgtctact tgaccgtcac caaggagtcc ggcaacagca
 961 tcgtgctcct gtttaagatg atcagcacca gagcagccag cggcctctac cgagccatca
1021 ccgaaacaca tgcattctat aggtgtgaca cagtcaccag tgccgtcatg atgcagtaca
1081 gtcgcgacct gaagggccac ttggcgtctc tgtttctgaa cgaaaacatt aaccttggta
1141 agaaatacgt cttcgacatc aagagaacat ccaaagaggt ctatgaccat gccaggaggg
1201 ctctgtacaa cgccggcgtt gtggaccttg tctctcgaag tgaccagagc ccccccagct
1261 cacccctgaa gtcctcagac agcagcatga gctgcagcag ctgtgagggc ctcagctgcc
1321 agcagacccg ggtgctgcag gagaagctgc gcaagctgaa ggaagccatg ctgtgtatgg
1381 cgtgctgcga ggaggagatc aactccacct tctgcccctg cggccacact gtgtgctgcg
1441 agagctgtgc agcccagctg cagtcctgtc cggtctgcag atcccgtgtg gagcatgtcc
1501 agcacgtcta cctgcccacc cacaccagtc tcctcaatct gactgtcatc tgatgcgtcc
1561 tgcactcgat ggacaagcca tgtccccaca agctgcagta ttgtaaacta taagaataat
1621 aactttgtga agagctattt cactctcaac acccatctgc catgagacat tttcagaaac
1681 aaggaggaaa agaaaacaag aatgtgacca cacctcttcc gtgaggagaa gcaacaggcc
1741 ccatggccac caggaagaac tctgggacac ggacacattc cttgaacttt agggttggtt
1801 tttttttta atgatcaagt aaaggagtag atagaatcgt cttcgtcagt caagtggcaa
1861 catggcccaa ccgtgggcac cttttaggaa atgacgtcat atgtctcctt cacttttcc
1921 ccgggcagca gattttgtaa gtgttttaag gatttccttg gttcttttg tatggtcatg
1981 gagcgctgaa tatttttaat agggattttt tttcttaaag aaatagtcct cattataaaa
2041 gtcatttctg tctttataac tcattcaaga acaactggaa aagctggcag attgaaaaaa
2101 aaaaagcaat cctgtgactt cccaagggtt gacagcaatg ttgtcagatt ggaagcagtc
2161 tggctgagag ccaataggta actcaccgtg ggtgacttcc ttcctagagc ccttccgttt
2221 cccctcattc cacaccccat gcctttcact gataaaaatg ctaccagttt ggttaagaga
2281 catacatggt agagtcaagc actccctggg ctttggagat tggaaagcga gagtagcttc
2341 cttgaaggaa aaagatgaga gagagagaga gagagagaga gagagagaga gagagagaga
2401 gagagagaga tgagccagag agccactcag tatgcccgag tggttcttca ctttcccaag
2461 cactcactcc agctgcaccc atgggtgtcg ccttgcttga agatcaaact ttctacagcc
2521 ttataggttt ctagatagtg tctccttttt gtgtatgtct tgtttctcgt tgttcgagtt
2581 ttcctatgtc agtgcttcca tactcattgt cctgcccccc cggtgtcttc cagaggtagg
2641 gctacttctt tatgtttcca tattctaagt tttcaccccc acttgggcat tttggaagct
2701 agtgagctag ggggtttttct agggtgtcag gaaacctagc tgacctcatc gggtgcaata
2761 ctagctaagt taaagctaga agcctacact gtcactttac tgagatttct gagtctacgt
2821 ttcatattgc cttaatgtag cagtaatgtg tttatgcatt tgtttctttg cacagacatt
2881 ttgtcagata ttaaaactct acttttttat ggcacatatt agcatataag cctttattcc
2941 aagaggtatt tatttttttca cttgtaaaaa aaataatgtt tcc
```

Figure 3. SEQ ID NO. 646 (Mouse Mylip/Idol mRNA Sequence; isoform 2)

```
   1 atgctgtgct atgtgacgag gccggacgcg gtgctgatgg aggtagaggt ggaggcaaaa
  61 gccaacggcg aggactgtct caaccaggtg tgcaggcgtc tagggatcat cgaggttgat
 121 tattttgggc tgcagttcac ggggagcaaa ggtgagagct tatggctgaa tctgagaaac
 181 cggatctccc agcagatgga tgggctggca ccttaccgcc ttaaactgag ggtcaagttc
 241 tttgtggagc ctcatctcat cttacaggag cagacaaggc atatcttttt cttgcacatt
 301 aaagagtccc tcttggcagg ccacctccag tgttccccag agcaggccgt ggaactcagt
 361 gccctcctgg ctcagaccaa atttggagac tacaaccaga acaccgccca atacagctat
 421 gaggacctgt gtgagaaaga gctctccagc tccactttga acagcatcgt tgcgaagcat
 481 aaggagctgg agggcatcag ccaggcctct gccgagtacc aggttctgca gattgtgtca
 541 gcgatggaga actacggcat agagtggcat gctgtgaggg acagcgaagg acagaaactc
 601 ctcattgggg tcggacctga aggcatctcg atctgtaaag aggactttag ccctattaac
 661 aggatagctt atcctgtggt gcagatggcc acccagtcag gaaagaatgt ctacttgacc
 721 gtcaccaagg agtccggcaa cagcatcgtg ctcctgttta agatgatcag caccagagca
 781 gccagcggcc tctaccgagc catcaccgaa acacatgcat tctataggtg tgacacagtc
 841 accagtgccg tcatgatgca gtacagtcgc gacctgaagg gccacttggc gtctctgttt
 901 ctgaacgaaa acattaacct tggtaagaaa tacgtcttcg acatcaagag aacatccaaa
 961 gaggtctatg accatgccag gagggctctg tacaacgccg gcgttgtgga ccttgtctct
1021 cgaagtgacc agagcccccc cagctcaccc ctgaagtcct cagacagcag catgagctgc
1081 agcagctgtg agggcctcag ctgccagcag acccgggtgc tgcaggagaa gctgcgcaag
1141 ctgaaggaag ccatgctgtg tatggcgtgc tgcgaggagg agatcaactc caccttctgc
1201 ccctgcggcc acactgtgtg ctgcgagagc tgtgcagccc agctgcagtc ctgtccggtc
1261 tgcagatccc gtgtggagca tgtccagcac gtctacctgc ccacccacac cagtctcctc
1321 aatctgactg tcatctga
```

Figure 4. SEQ ID NO. 647 (Rat Mylip/Idol mRNA Sequence)

```
   1 cagtggggct gtcggagcgg cgcggccgtg tagctcccgg gaactggctg tcgtgggggg
  61 tggcggggac gcgagtggcg gctgcgtggg gtgcagggcg ggtgaccgca cggctgcacc
 121 ttcctcgcgg tgcccggagc cgacttggag caattgcagt gaggcgacag ccccggcgca
 181 caccggagaa gaagcggccg tggcggcggt ggcggcggcc ccagccatgc tgtgctatgt
 241 gacgaggccg gacgcggtgc tgatggaggt ggaggtggag gcaaaagcca acggcgagga
 301 ctgtctcaac caggtgtgca ggcgattggg aatcatagaa gttgattatt ttgggctgca
 361 gttcacgggt agcaaaggtg aaagcttatg gctgaatctg agaaaccgga tctcccagca
 421 gatggatggg ctggcacctt accggcttaa actgagggtc aagttctttg tggagcccca
 481 tctcatctta caggagcaga caaggcatat ctttttcttg cacattaaag agtccctctt
 541 ggcaggccac ctccagtgtt ccccagagca ggcagtggaa cttagtgccc tcctggccca
 601 gaccaaattc ggagactaca accagaacac tgcccaatac agctatgagg acctgtgtga
 661 gaaagagctc tccagctcca cattgaacag cattgttggg aagcataagg agctggaggg
 721 catcagccag gcttctgcag aataccaagt tctgcagatt gtgtcagcaa tggagaacta
 781 cggcatagag tggcatgccg tgagggacag cgaaggacag aaactcctca ttggggtcgg
 841 acctgaaggc atctcaattt gtaaagagga ctttagccct attaacagga tagcttatcc
 901 tgtggtgcag atggccaccc agtcaggaaa gaatgtctac ttgaccgtca ccaaggagtc
 961 cggtaacagc atcgtgctcc tgtttaaaat gatcagcacc cgagctgcca gtgggctcta
1021 ccgagctatc acggaaacac atgcattcta caggcgcgtg tgacacagtc accagtgccg
1081 tcatgatgca gtacagtcgt gacttgaagg gccacttggc gtctctgttt ctgaatgaga
1141 acattaatct tggcaagaaa tatgtctttg atattaaaag aacatccaaa gaggtatatg
1201 accatgccag gagggctctg tacaacgccg gtgttgtgga ccttgtctct cgaaatgacc
1261 agagccctcc cagctcgcct ctgaagtcct ctgacagcag catgagctgc agcagctgcg
1321 agggcctcag ctgccagcag accagagtgc tgcaggagaa gctgcgcaaa ctgaaggaag
1381 ccatgctgtg catggtgtgc tgcgaggagg agatcaactc tacctttgc ccctgtggcc
1441 atactgtgtg ctgtgagagc tgtgcagccc agctgcagtc atgtcccgtc tgcagatcac
1501 gtgtggaaca tgtccagcac gtctacctgc ccacccacac cagtcttctc aatctgactg
1561 tcatctaatg cgtcctgtgc ttactgggca tgccatgtcc ccacaagctg cagtattgta
1621 aactagaaga agagtaactc tgtgaagaaa tagttcactc tcaacaccca tttgccatga
1681 gacgtttcca gaaacgagga ggaaaggaaa gaatgcgacc acacctcttc tgtgaggaga
1741 agcaacagtt cccatggcaa ccaggaagag atctggaaca tggacacatt ccttgggctt
1801 tggggttttt ttaatgatca agtaaaggag tagataaaat tgtctctgtc agtcaagtgg
1861 caacatggcc caaccgtggg cacctttaag gaaatgatgt catatgtctc cttcacttgt
1921 cccgaggcag cagattttgt aagagtttta aggatttcct tggttctttt tgtatggtca
1981 tggagcgctg aacatttttа ataggatttt ttttttttg tcttaaagaa atagtcctca
2041 ttagaaagtc atttctgtct ttataactca ttcaagaaca actggaaagc tggtagtttg
2101 gaaagcaatc ccgtgacttc tcaagggttg agagcaacgt ggtcagattg gaaccagtct
2161 ggctgagagt caacaggtaa cccaccgtgg gtgacttcgc tcctagctcc cctgtttccc
2221 tcactccaca tcccatgcct ttcactgata aaaatgctac cagtttggtt acatacatgg
2281 catggtcaag cactccctgg gctttggagc tagtggacta tttgcagatc ggaaagggag
2341 agtggcagag aggcttcctt ggaagggaag gggggggggag agagagagaa agagagagag
2401 agagagagag agagagagag gggagccaga gagccagagt gagttttcac ttcccccaag
2461 cactcactcc agcagcaccc atgggtgtcg ccgtgcttga agatcaaact ttctacagcc
2521 ttataggttt ctaggttgta tctcctcttt gtgtctgtct taattccctt tgttggtgtt
2581 ttcttaggtc agtgcttccg tattcattgt actgcctcct cggcatcttc cagaggtggg
2641 gccacttcat tatgtttcta tattcttcgt cataatttca cccccacttg ggcattttgg
2701 aagctagtga gctagggggt tttctagggt gtccggaagc ctagctgacc tcatcgggtg
2761 caatactagc tacattaaag ctagaaacct acactgtcac tttactgagc tctgagtcta
2821 cgtttcatat tgccttaatg tagcagtaat gtgtttatgc atttgtttct ttgcacagac
2881 attttgtcag atattaaaac tctacttttt tatggcacat attagcatat aagcctttat
2941 tccaagaggt atttatttttt tcacttgtaa aaaaaaataa tgtttccaca tttaaaaaaa
3001 aatcaactct gttatatcct agaggacttc tgtcttttat attcaggata ataaagactt
3061 taaagc
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COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF MYLIP/IDOL GENE

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a 35 U.S.C. §371 National Phase Entry Application of International Application No. PCT/US2011/22339, filed Jan. 25, 2011, which designates the United States, and which claims benefit under 35 U.S.C. §119(*e*) of U.S. provisional application 61/297,954 filed on Jan. 25, 2010, the contents of which are incorporated herein in their entireties by reference.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Jul. 23, 2012, is named 20120725_SequenceListing-TextFile__051058__054000_US.txt and is 373,982 bytes in size.

FIELD OF THE INVENTION

The invention relates to the specific inhibition of the expression of the Mylip/Idol gene.

BACKGROUND OF THE INVENTION

Myosin Regulatory light chain interacting protein (Mylip) is an ERM-like protein that interacts with myosin regulatory light chain and inhibits neurite outgrowth in neurons. The Mylip protein comprises a FERM homology domain at the N-terminus, and a RING zinc finger ubiquitin ligase domain at the C-terminus. While FERM-containing proteins are known to interact with the cytoplasmic regions of transmembrane proteins, Mylip is presently the only FERM-containing protein known to interact with the myosin regulatory light chain protein. Mylip is expressed ubiquitously in almost all human tissues.

Mylip has been shown to downregulate the LDL receptor by enhancing LDL receptor ubiquitination and leading to degradation of the LDL receptor (LDL-R). Overexpression of the Mylip protein in mice reduces levels of the LDL-R, decreases LDL uptake into cells and increases plasma cholesterol levels. Conversely, inhibition of Mylip expression in mice enhances LDL uptake into cells. Given the actions of Mylip on LDL-R expression, the protein is also referred to as 'inducible degrador of the LDL-R' (Idol).

Autosomal dominant hypercholesterolemias (ADHs) are monogenic diseases in which patients exhibit elevated total and LDL cholesterol levels, tendon xanthomas, and premature atherosclerosis (Rader, D. J., (2003) J. Clin. Invest. 111, 1795-1803). The pathogenesis of ADHs and a recessive form, autosomal recessive hypercholesterolemia (ARH) (Cohen, J. C., (2003) Curr. Opin. Lipidol. 14, 121-127), is due to defects in LDL uptake by the liver. ADH may be caused by LDLR mutations, which prevent LDL uptake, or by mutations in the protein on LDL, apolipoprotein B, which binds to the LDLR. ARH is caused by mutations in the ARH protein that are necessary for endocytosis of the LDLR-LDL complex via its interaction with clathrin. As Mylip/Idol plays a role in receptor-mediated LDL uptake it is likely that treatment strategies directed at Mylip/Idol would be beneficial in the above-described disorders.

SUMMARY OF THE INVENTION

Described herein are compositions and methods that effect the RNA-induced silencing complex (RISC)-mediated cleavage of RNA transcripts of the Mylip/Idol gene, such as in a cell or mammal. Also described are compositions and methods for treating pathological conditions and diseases caused by the expression of a Mylip/Idol gene, such as a lipid disorder or metabolic disorder (e.g., atherosclerosis or diabetes). Also described are compositions and methods described for promoting neurite outgrowth, thus permitting treatment of neurodegenerative disorders or nerve damage such as e.g., spinal cord injury.

As used herein, the term "iRNA" refers to an agent that contains RNA as that term is defined herein, and which mediates the targeted cleavage of an RNA transcript via an RNA-induced silencing complex (RISC) pathway. In one embodiment, an iRNA as described herein inhibits the expression of Mylip/Idol in a cell or mammal. Alternatively, in another embodiment, the iRNA up-regulates the expression of Mylip/Idol in a cell or mammal.

The iRNAs included in the compositions featured herein encompass a dsRNA having an RNA strand (the antisense strand) having a region that is 30 nucleotides or less, generally 19-24 nucleotides in length, that is substantially complementary to at least part of an mRNA transcript of a Mylip/Idol gene. In one embodiment, the dsRNA comprises a region of at least 15 contiguous nucleotides.

In one embodiment, an iRNA for inhibiting expression of a Mylip/Idol gene includes at least two sequences that are complementary to each other. The iRNA includes a sense strand having a first sequence and an antisense strand having a second sequence. The antisense strand includes a nucleotide sequence that is substantially complementary to at least part of an mRNA encoding Mylip/Idol, and the region of complementarity is 30 nucleotides or less, and at least 15 nucleotides in length. Generally, the iRNA is 19 to 24, e.g., 19 to 21 nucleotides in length. In some embodiments the iRNA is from about 15 to about 25 nucleotides in length, and in other embodiments the iRNA is from about 25 to about 30 nucleotides in length. The iRNA, upon contacting with a cell expressing Mylip/Idol, inhibits the expression of a Mylip/Idol gene by at least 10%, at least 20%, at least 25%, at least 30%, at least 35% or at least 40% or more, such as when assayed by a method as described herein. In one embodiment, the Mylip/Idol iRNA is formulated in a stable nucleic acid lipid particle (SNALP).

In one embodiment, an iRNA featured herein includes a first sequence of a dsRNA that is selected from the group consisting of the sense sequences of Tables 3, 4, 5 and 6, and a second sequence that is selected from the group consisting of the corresponding antisense sequences of Tables 3, 4, 5 and 6. The iRNA molecules featured herein can include naturally occurring nucleotides or can include at least one modified nucleotide, including, but not limited to a 2'-O-methyl modified nucleotide, a nucleotide having a 5'-phosphorothioate group, and a terminal nucleotide linked to a cholesteryl derivative. Alternatively, the modified nucleotide may be chosen from the group of: a 2'-deoxy-2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a locked nucleotide, an abasic nucleotide, 2'-amino-modified nucleotide, 2'-alkyl-modified nucleotide, morpholino nucleotide, a phosphoramidate, and a non-natural base comprising nucleotide. Generally, such a modified sequence will be based on a first sequence of said iRNA selected from the group consisting of the sense sequences of Tables 3, 4, 5 and 6, and a second

sequence selected from the group consisting of the antisense sequences of Tables 3, 4, 5 and 6.

In another embodiment, a composition containing a dsRNA targeting Mylip/Idol is administered to a subject when Low Density Lipoprotein cholesterol (LDLc) levels reach or surpass a predetermined minimal level, such as greater than 130 mg/dL, 150 mg/dL, 200 mg/dL, 300 mg/dL, or 400 mg/dL. In another embodiment, the subject has an LDLc level greater than about 150 mg/dL.

In one embodiment, a single administration of the dsRNA lowers LDLc levels by at least 10%, e.g., by at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, or at least 60%, or more. In another embodiment, the lowered LDLc level is maintained for at least 5, 10, 20, 30, or 40 days or longer.

In one embodiment, the subject is selected, at least in part, on the basis of needing (as opposed to merely selecting a patient on the grounds of who happens to be in need of) LDL lowering, LDL lowering without lowering of HDL, ApoB lowering, or total cholesterol lowering without HDL lowering.

In one embodiment, an iRNA as described herein targets a wildtype Mylip/Idol RNA transcript, and in another embodiment, the iRNA targets a mutant transcript (e.g., a Mylip/Idol RNA carrying an allelic variant). For example, an iRNA of the invention can target a polymorphic variant, such as a single nucleotide polymorphism (SNP), of Mylip/Idol. In another embodiment, the iRNA targets both a wildtype and a mutant Mylip/Idol transcript. In yet another embodiment, the iRNA targets a transcript variant of Mylip/Idol.

In one embodiment, an iRNA featured in the invention targets a non-coding region of a Mylip/Idol RNA transcript, such as the 5' or 3' untranslated region.

In one aspect, embodiments of the invention provide a cell containing at least one of the iRNAs featured in the invention. The cell is generally a mammalian cell, such as a human cell.

In another aspect, embodiments of the invention provide a pharmaceutical composition for inhibiting the expression of a Mylip/Idol gene in an organism, generally a human subject. The composition typically includes one or more of the iRNAs described herein and a pharmaceutically acceptable carrier or delivery vehicle. In one embodiment, the composition is used for treating a lipid disorder, such as atherosclerosis. In another embodiment, the composition is used for treating a spinal cord injury or a neurodegenerative disease or disorder, such as palsy, or Parkinson's disease.

In another embodiment, the pharmaceutical composition is formulated for administration of a dosage regimen described herein, e.g., not more than once every four weeks, not more than once every three weeks, not more than once every two weeks, or not more than once every week. In another embodiment, the administration of the pharmaceutical composition can be maintained for a month or longer, e.g., one, two, three, or six months, or one year, or five years, or ten years, or longer, including the remaining lifetime of a subject.

In another embodiment, a composition containing an iRNA described herein, e.g., a dsRNA targeting Mylip/Idol, is administered with a non-iRNA therapeutic agent, such as an agent known to treat a lipid disorder, or a symptom of a lipid disorder. For example, an iRNA featured in the invention can be administered with an agent for treatment of atherosclerosis or hypercholesterolemia or other disorders associated with cholesterol metabolism.

In another embodiment, a Mylip/Idol iRNA is administered to a patient, and then the non-iRNA agent is administered to the patient (or vice versa). In another embodiment, a Mylip/Idol iRNA and the non-iRNA therapeutic agent are administered at the same time. In one embodiment, the agent is, for example, an agent that affects cholesterol metabolism, such as an HMG-CoA reductase inhibitor (e.g., a statin).

In another aspect, provided herein is a method for inhibiting the expression of a Mylip/Idol gene in a cell by performing the following steps:

(a) introducing into the cell a double-stranded ribonucleic acid (dsRNA), wherein the dsRNA includes at least two sequences that are complementary to each other. The dsRNA has a sense strand having a first sequence and an antisense strand having a second sequence; the antisense strand has a region of complementarity that is substantially complementary to at least a part of an mRNA encoding Mylip/Idol, and where the region of complementarity is 30 nucleotides or less, i.e., 15-30 nucleotides in length, and generally 19-24 nucleotides in length, and where the dsRNA, upon contact with a cell expressing Mylip/Idol, inhibits expression of a Mylip/Idol gene by at least 10%, preferably at least 20%, at least 30%, at least 40% or more; and

(b) maintaining the cell produced in step (a) for a time sufficient to obtain degradation of the mRNA transcript of the Mylip/Idol gene, thereby inhibiting expression of a Mylip/Idol gene in the cell.

In another aspect, the invention provides methods and compositions useful for activating expression of a Mylip/Idol gene in a cell or mammal.

In another aspect, the invention provides a method for modulating the expression of a Mylip/Idol gene in a cell by performing the following steps:

(a) introducing into the cell a double-stranded ribonucleic acid (dsRNA), wherein the dsRNA includes at least two sequences that are complementary to each other. The dsRNA has a sense strand having a first sequence and an antisense strand having a second sequence; the antisense strand has a region of complementarity that is substantially complementary to at least a part of an mRNA encoding Mylip/Idol, and where the region of complementarity is 30 nucleotides or less, i.e., 15-30 nucleotides in length, and generally 19-24 nucleotides in length, and where the dsRNA, upon contact with a cell expressing Mylip/Idol, modulates expression of a Mylip/Idol gene by at least 10%, preferably at least 20%, at least 30%, at least 40% or more; and

(b) maintaining the cell produced in step (a) for a time sufficient to obtain degradation or protection of the mRNA transcript of the Mylip/Idol gene, thereby modulating expression of a Mylip/Idol gene in the cell.

In one embodiment, the method is for inhibiting gene expression in a macrophage, a fibroblast, or a liver cell. In another embodiment, the method is for activating gene expression in a macrophage, a fibroblast, or a liver cell.

In another embodiment, the method is for inhibiting gene expression in a neuronal cell. In another embodiment, the method is for activating gene expression in a neuronal cell.

In other aspects, the invention provides methods for treating, preventing, reversing, or managing pathological processes mediated by Mylip/Idol expression, such as a lipid disorder. In one embodiment, the method includes administering to a patient in need of such treatment, prevention, reversal, or management a therapeutically or prophylactically effective amount of one or more of the iRNAs featured in the invention. In one embodiment the patient has diabetes or atherosclerosis. In another embodiment, administration of the iRNA targeting Mylip/Idol alleviates or relieves the severity of at least one symptom of a Mylip/Idol-mediated disorder in the patient, such as high LDLc level, high ApoB level, or high

total cholesterol level. In another embodiment, administration of the Mylip/Idol dsRNA does not lower the level of HDL cholesterol in the patient. In another embodiment, administration of the Mylip/Idol dsRNA increases neurite outgrowth and/or reduces at least one symptom of a neurodegenerative disease.

In one aspect, the invention provides a vector for inhibiting the expression of a Mylip/Idol gene in a cell. In one embodiment, the vector includes at least one regulatory sequence operably linked to a nucleotide sequence that encodes at least one strand of an iRNA as described herein.

In another aspect, the invention provides a cell containing a vector for inhibiting the expression of a Mylip/Idol gene in a cell. The vector includes a regulatory sequence operably linked to a nucleotide sequence that encodes at least one strand of one of the iRNAs as described herein.

In yet another aspect, the invention provides a composition containing a Mylip/Idol iRNA, in combination with a second iRNA targeting a second gene involved in a pathological disease, and useful for treating the disease, e.g., a lipid disorder, metabolic disorder or neurodegenerative disorder.

The details of various embodiments of the invention are set forth in the description below. Other features, objects, and advantages of the invention will be apparent from the description and the drawings, and from the claims.

DESCRIPTION OF THE DRAWINGS

FIG. **1** is the sequence of human Mylip/Idol mRNA (Ref. Seq. NM_013262.3, SEQ ID NO: 644).

FIG. **2** is a sequence of mouse Mylip/Idol mRNA, isoform 1 (Ref. Seq. NM_153789.3; SEQ ID NO: 645).

FIG. **3** is a sequence of mouse Mylip/Idol mRNA, isoform 2 (Ref. Seq. NM_181043.1; SEQ ID NO: 646).

FIG. **4** is a sequence of rat Mylip/Idol mRNA (Ref. Seq. NM_001107344.1; SEQ ID NO: 647).

DETAILED DESCRIPTION OF THE INVENTION

Described herein are iRNAs and methods of using them for inhibiting the expression of a Mylip/Idol gene in a cell or a mammal where the iRNA targets a Mylip/Idol gene. Also provided are compositions and methods for treating pathological conditions and diseases, such as a lipid disorder, neurodegenerative disease, or a metabolic disorder, in a mammal caused by the expression of a Mylip/Idol gene. iRNA directs the sequence-specific degradation of mRNA through a process known as RNA interference (RNAi). In one embodiment, the iRNA activates the expression of a Mylip/Idol gene in a cell or mammal, where the iRNA targets a Mylip/Idol gene.

Double-stranded RNA molecules (dsRNA) have been shown to block gene expression in a highly conserved regulatory mechanism known as RNA interference (RNAi). WO 99/32619 (Fire et al.) disclosed the use of a dsRNA of at least 25 nucleotides in length to inhibit the expression of genes in *C. elegans*. dsRNA has also been shown to degrade target RNA in other organisms, including plants (see, e.g., WO 99/53050, Waterhouse et al.; and WO 99/61631, Heifetz et al.), *Drosophila* (see, e.g., Yang, D., et al., *Curr. Biol.* (2000) 10:1191-1200), and mammals (see WO 00/44895, Limmer; and DE 101 00 586.5, Kreutzer et al.). This natural mechanism has now become the focus for the development of a new class of pharmaceutical agents for treating disorders that are caused by the aberrant or unwanted regulation of a gene.

The iRNAs of the compositions described herein include an RNA strand (the antisense strand) having a region which is 30 nucleotides or less in length, i.e., 15-30 nucleotides in length, generally 19-24 nucleotides in length, which region is substantially complementary to at least part of an mRNA transcript of a Mylip/Idol gene. The use of these iRNAs enables the targeted degradation of mRNAs of genes that are implicated in pathologies associated with Mylip/Idol expression in mammals. Very low dosages of Mylip/Idol iRNAs in particular can specifically and efficiently mediate RNAi, resulting in significant inhibition of expression of a Mylip/Idol gene. Using cell-based assays, the present inventors have demonstrated that iRNAs targeting Mylip/Idol can specifically and efficiently mediate RNAi, resulting in significant inhibition of expression of a Mylip/Idol gene. Thus, methods and compositions including these iRNAs are useful for treating pathological processes that can be mediated by down regulating Mylip/Idol, such as in the treatment of a lipid disorder, e.g., atherosclerosis, and hypercholesterolemia. The following detailed description discloses how to make and use compositions containing iRNAs to inhibit the expression of a Mylip/Idol gene, as well as compositions and methods for treating diseases and disorders caused by the expression of this gene.

Embodiments of the pharmaceutical compositions featured herein also include an iRNA having an antisense strand comprising a region which is 30 nucleotides or less in length, generally 19-24 nucleotides in length, which region is substantially complementary to at least part of an RNA transcript of a Mylip/Idol gene, together with a pharmaceutically acceptable carrier. Embodiments of compositions featured in the invention also include an iRNA having an antisense strand having a region of complementarity which is 30 nucleotides or less in length, generally 19-24 nucleotides in length, and is substantially complementary to at least part of an RNA transcript of a Mylip/Idol gene.

Accordingly, in some aspects, pharmaceutical compositions containing a Mylip/Idol iRNA and a pharmaceutically acceptable carrier, methods of using the compositions to inhibit expression of a Mylip/Idol gene, and methods of using the pharmaceutical compositions to treat diseases caused by expression of a Mylip/Idol gene are featured in the invention.

I. Definitions

For convenience, the meaning of certain terms and phrases used in the specification, examples, and appended claims, are provided below. If there is an apparent discrepancy between the usage of a term in other parts of this specification and its definition provided in this section, the definition in this section shall prevail.

"G," "C," "A," "T" and "U" each generally stand for a nucleotide that contains guanine, cytosine, adenine, thymidine and uracil as a base, respectively. However, it will be understood that the term "ribonucleotide" or "nucleotide" can also refer to a modified nucleotide, as further detailed below, or a surrogate replacement moiety. The skilled person is well aware that guanine, cytosine, adenine, and uracil may be replaced by other moieties without substantially altering the base pairing properties of an oligonucleotide comprising a nucleotide bearing such replacement moiety. For example, without limitation, a nucleotide comprising inosine as its base may base pair with nucleotides containing adenine, cytosine, or uracil. Hence, nucleotides containing uracil, guanine, or adenine can be replaced in the nucleotide sequences of dsRNA featured herein by a nucleotide containing, for example, inosine. In another example, adenine and cytosine anywhere in the oligonucleotide can be replaced with guanine and uracil, respectively to form G-U Wobble base pairing

with the target mRNA. Sequences containing such replacement moieties are suitable for the compositions and methods described herein.

As used herein, "Myosin regulatory light chain interacting protein" ("Mylip") or "inducible degrador of the LDL-R" ("Idol") refers to a particular polypeptide expressed in a cell. Mylip is also known as Idol, Mylip/Idol, MIR (myosin regulatory light chain (MRLC) interacting protein) and MSAP. The sequence of a human Mylip/Idol mRNA transcript can be found at NM_013262.3 (SEQ ID NO: 644). The sequence of mouse Mylip/Idol mRNA can be found at NM_153789.3 (isoform 1; SEQ ID NO: 645) or NM_181043.1 (isoform 2; SEQ ID NO: 646), and the sequence of rat Mylip/Idol mRNA can be found at NM_001107344.1 (SEQ ID NO: 647). The mouse and rat sequences of Mylip/Idol are highly conserved.

As used herein, the term "iRNA" refers to an agent that contains RNA as that term is defined herein, and which mediates the targeted cleavage of an RNA transcript via an RNA-induced silencing complex (RISC) pathway. In one embodiment, an iRNA as described herein effects inhibition of Mylip/Idol expression. Alternatively, in another embodiment, an iRNA as described herein activates Mylip/Idol expression.

As used herein, "target sequence" refers to a contiguous portion of the nucleotide sequence of an mRNA molecule formed during the transcription of a Mylip/Idol gene, including messenger RNA (mRNA) that is a product of RNA processing of a primary transcription product. The target portion of the sequence will be at least long enough to serve as a substrate for iRNA-directed cleavage at or near that portion. For example, the target sequence will generally be from 9-36 nucleotides in length, e.g., 15-30 nucleotides in length, including all sub-ranges therebetween. As non-limiting examples, the target sequence can be from 15-30 nucleotides, 15-26 nucleotides, 15-23 nucleotides, 15-22 nucleotides, 15-21 nucleotides, 15-20 nucleotides, 15-19 nucleotides, 15-18 nucleotides, 15-17 nucleotides, 18-30 nucleotides, 18-26 nucleotides, 18-23 nucleotides, 18-22 nucleotides, 18-21 nucleotides, 18-20 nucleotides, 19-30 nucleotides, 19-26 nucleotides, 19-23 nucleotides, 19-22 nucleotides, 19-21 nucleotides, 19-20 nucleotides, 20-30 nucleotides, 20-26 nucleotides, 20-25 nucleotides, 20-24 nucleotides, 20-23 nucleotides, 20-22 nucleotides, 20-21 nucleotides, 21-30 nucleotides, 21-26 nucleotides, 21-25 nucleotides, 21-24 nucleotides, 21-23 nucleotides, or 21-22 nucleotides.

As used herein, the term "strand comprising a sequence" refers to an oligonucleotide comprising a chain of nucleotides that is described by the sequence referred to using the standard nucleotide nomenclature.

As used herein, and unless otherwise indicated, the term "complementary," when used to describe a first nucleotide sequence in relation to a second nucleotide sequence, refers to the ability of an oligonucleotide or polynucleotide comprising the first nucleotide sequence to hybridize and form a duplex structure under certain conditions with an oligonucleotide or polynucleotide comprising the second nucleotide sequence, as will be understood by the skilled person. Such conditions can, for example, be stringent conditions, where stringent conditions may include: 400 mM NaCl, 40 mM PIPES pH 6.4, 1 mM EDTA, 50° C. or 70° C. for 12-16 hours followed by washing. Other conditions, such as physiologically relevant conditions as can be encountered inside an organism, can apply. The skilled person will be able to determine the set of conditions most appropriate for a test of complementarity of two sequences in accordance with the ultimate application of the hybridized nucleotides.

Complementary sequences within an iRNA, e.g., within a dsRNA as described herein, include base-pairing of the oligonucleotide or polynucleotide comprising a first nucleotide sequence to an oligonucleotide or polynucleotide comprising a second nucleotide sequence over the entire length of one or both nucleotide sequences. Such sequences can be referred to as "fully complementary" with respect to each other herein. However, where a first sequence is referred to as "substantially complementary" with respect to a second sequence herein, the two sequences can be fully complementary, or they can form one or more, but generally not more than 5, 4, 3 or 2 mismatched base pairs upon hybridization for a duplex up to 30 base pairs (bp), while retaining the ability to hybridize under the conditions most relevant to their ultimate application, e.g., inhibition of gene expression via a RISC pathway. However, where two oligonucleotides are designed to form, upon hybridization, one or more single stranded overhangs, such overhangs shall not be regarded as mismatches with regard to the determination of complementarity. For example, a dsRNA comprising one oligonucleotide 21 nucleotides in length and another oligonucleotide 23 nucleotides in length, wherein the longer oligonucleotide comprises a sequence of 21 nucleotides that is fully complementary to the shorter oligonucleotide, may yet be referred to as "fully complementary" for the purposes described herein.

"Complementary" sequences, as used herein, can also include, or be formed entirely from, non-Watson-Crick base pairs and/or base pairs formed from non-natural and modified nucleotides, in as far as the above requirements with respect to their ability to hybridize are fulfilled. Such non-Watson-Crick base pairs includes, but are not limited to, G:U Wobble or Hoogstein base pairing.

The terms "complementary," "fully complementary" and "substantially complementary" herein can be used with respect to the base matching between the sense strand and the antisense strand of a dsRNA, or between the antisense strand of an iRNA agent and a target sequence, as will be understood from the context of their use.

As used herein, a polynucleotide that is "substantially complementary to at least part of" a messenger RNA (an mRNA) refers to a polynucleotide that is substantially complementary to a contiguous portion of the mRNA of interest (e.g., an mRNA encoding Mylip/Idol). For example, a polynucleotide is complementary to at least a part of a Mylip/Idol mRNA if the sequence is substantially complementary to a non-interrupted portion of an mRNA encoding Mylip/Idol.

The term "double-stranded RNA" or "dsRNA," as used herein, refers to an iRNA that includes an RNA molecule or complex of molecules having a hybridized duplex region that comprises two anti-parallel and substantially complementary nucleic acid strands, which will be referred to as having "sense" and "antisense" orientations with respect to a target RNA. The duplex region can be of any length that permits specific degradation of a desired target RNA through a RISC pathway, but will typically range from 9 to 36 base pairs in length, e.g., 15-30 base pairs in length. Considering a duplex between 9 and 36 base pairs, the duplex can be any length in this range, for example, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 and any sub-range therein between, including, but not limited to 15-30 base pairs, 15-26 base pairs, 15-23 base pairs, 15-22 base pairs, 15-21 base pairs, 15-20 base pairs, 15-19 base pairs, 15-18 base pairs, 15-17 base pairs, 18-30 base pairs, 18-26 base pairs, 18-23 base pairs, 18-22 base pairs, 18-21 base pairs, 18-20 base pairs, 19-30 base pairs, 19-26 base pairs, 19-23 base pairs, 19-22 base pairs, 19-21 base pairs, 19-20 base pairs, 20-30 base pairs, 20-26 base pairs, 20-25 base pairs, 20-24 base pairs, 20-23 base pairs,

20-22 base pairs, 20-21 base pairs, 21-30 base pairs, 21-26 base pairs, 21-25 base pairs, 21-24 base pairs, 21-23 base pairs, or 21-22 base pairs. dsRNAs generated in the cell by processing with Dicer and similar enzymes are generally in the range of 19-22 base pairs in length. One strand of the duplex region of a dsDNA comprises a sequence that is substantially complementary to a region of a target RNA. The two strands forming the duplex structure can be from a single RNA molecule having at least one self-complementary region, or can be formed from two or more separate RNA molecules. Where the duplex region is formed from two strands of a single molecule, the molecule can have a duplex region separated by a single stranded chain of nucleotides (herein referred to as a "hairpin loop") between the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure. The hairpin loop can comprise at least one unpaired nucleotide; in some embodiments the hairpin loop can comprise at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 20, at least 23 or more unpaired nucleotides. Where the two substantially complementary strands of a dsRNA are comprised by separate RNA molecules, those molecules need not, but can be covalently connected. Where the two strands are connected covalently by means other than a hairpin loop, the connecting structure is referred to as a "linker." The term "siRNA" is also used herein to refer to a dsRNA as described above.

The skilled artisan will recognize that the term "RNA molecule" or "ribonucleic acid molecule" encompasses not only RNA molecules as expressed or found in nature, but also analogs and derivatives of RNA comprising one or more ribonucleotide/ribonucleoside analogs or derivatives as described herein or as known in the art. Strictly speaking, a "ribonucleoside" includes a nucleoside base and a ribose sugar, and a "ribonucleotide" is a ribonucleoside with one, two or three phosphate moieties. However, the terms "ribonucleoside" and "ribonucleotide" can be considered to be equivalent as used herein. The RNA can be modified in the nucleobase structure or in the ribose-phosphate backbone structure, e.g., as described herein below. However, the molecules comprising ribonucleoside analogs or derivatives must retain the ability to form a duplex. As non-limiting examples, an RNA molecule can also include at least one modified ribonucleoside including but not limited to a 2'-O-methyl modified nucleoside, a nucleoside comprising a 5' phosphorothioate group, a terminal nucleoside linked to a cholesteryl derivative or dodecanoic acid bisdecylamide group, a locked nucleoside, an abasic nucleoside, a 2'-deoxy-2'-fluoro modified nucleoside, a 2'-amino-modified nucleoside, 2'-alkyl-modified nucleoside, morpholino nucleoside, a phosphoramidate or a non-natural base comprising nucleoside, or any combination thereof. Alternatively, an RNA molecule can comprise at least two modified ribonucleosides, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20 or more, up to the entire length of the dsRNA molecule. The modifications need not be the same for each of such a plurality of modified ribonucleosides in an RNA molecule. In one embodiment, modified RNAs contemplated for use in methods and compositions described herein are peptide nucleic acids (PNAs) that have the ability to form the required duplex structure and that permit or mediate the specific degradation of a target RNA via a RISC pathway.

In one aspect, a modified ribonucleoside includes a deoxyribonucleoside. In such an instance, an iRNA agent can comprise one or more deoxynucleosides, including, for example, a deoxynucleoside overhang(s), or one or more deoxynucleosides within the double stranded portion of a dsRNA. However, it is self evident that under no circumstances is a double stranded DNA molecule encompassed by the term "iRNA."

In one aspect, an RNA interference agent includes a single stranded RNA that interacts with a target RNA sequence to direct the cleavage of the target RNA. Without wishing to be bound by theory, long double stranded RNA introduced into plants and invertebrate cells is broken down into siRNA by a Type III endonuclease known as Dicer (Sharp et al., Genes Dev. 2001, 15:485). Dicer, a ribonuclease-III-like enzyme, processes the dsRNA into 19-23 base pair short interfering RNAs with characteristic two base 3' overhangs (Bernstein, et al., (2001) Nature 409:363). The siRNAs are then incorporated into an RNA-induced silencing complex (RISC) where one or more helicases unwind the siRNA duplex, enabling the complementary antisense strand to guide target recognition (Nykanen, et al., (2001) Cell 107:309). Upon binding to the appropriate target mRNA, one or more endonucleases within the RISC cleaves the target to induce silencing (Elbashir, et al.,(2001) Genes Dev. 15:188). Thus, in one aspect the invention relates to a single stranded RNA that promotes the formation of a RISC complex to effect silencing of the target gene.

As used herein, the term "nucleotide overhang" refers to at least one unpaired nucleotide that protrudes from the duplex structure of an iRNA, e.g., a dsRNA. For example, when a 3'-end of one strand of a dsRNA extends beyond the 5'-end of the other strand, or vice versa, there is a nucleotide overhang. A dsRNA can comprise an overhang of at least one nucleotide; alternatively the overhang can comprise at least two nucleotides, at least three nucleotides, at least four nucleotides, at least five nucleotides or more. A nucleotide overhang can comprise or consist of a nucleotide/nucleoside analog, including a deoxynucleotide/nucleoside. The overhang(s) may be on the sense strand, the antisense strand or any combination thereof. Furthermore, the nucleotide(s) of an overhang can be present on the 5' end, 3' end or both ends of either an antisense or sense strand of a dsRNA.

In one embodiment, the antisense strand of a dsRNA has a 1-10 nucleotide overhang at the 3' end and/or the 5' end. In one embodiment, the sense strand of a dsRNA has a 1-10 nucleotide overhang at the 3' end and/or the 5' end. In another embodiment, one or more of the nucleotides in the overhang is replaced with a nucleoside thiophosphate.

The terms "blunt" or "blunt ended" as used herein in reference to a dsRNA mean that there are no unpaired nucleotides or nucleotide analogs at a given terminal end of a dsRNA, i.e., no nucleotide overhang. One or both ends of a dsRNA can be blunt. Where both ends of a dsRNA are blunt, the dsRNA is said to be blunt ended. To be clear, a "blunt ended" dsRNA is a dsRNA that is blunt at both ends, i.e., no nucleotide overhang at either end of the molecule. Most often such a molecule will be double-stranded over its entire length.

The term "antisense strand" or "guide strand" refers to the strand of an iRNA, e.g., a dsRNA, which includes a region that is substantially complementary to a target sequence. As used herein, the term "region of complementarity" refers to the region on the antisense strand that is substantially complementary to a sequence, for example a target sequence, as defined herein. Where the region of complementarity is not fully complementary to the target sequence, the mismatches may be in the internal or terminal regions of the molecule. Generally, the most tolerated mismatches are in the terminal regions, e.g., within 5, 4, 3, or 2 nucleotides of the 5' and/or 3' terminus.

The term "sense strand," or "passenger strand" as used herein, refers to the strand of an iRNA that includes a region

that is substantially complementary to a region of the antisense strand as that term is defined herein.

As used herein, in one embodiment, the term "SNALP" refers to a stable nucleic acid-lipid particle. A SNALP represents a vesicle of lipids coating a reduced aqueous interior comprising a nucleic acid such as an iRNA or a plasmid from which an iRNA is transcribed. SNALPs are described, e.g., in U.S. Patent Application Publication Nos. 20060240093, 20070135372, and in International Application No. WO 2009082817. Examples of "SNALP" formulations are described elsewhere herein.

"Introducing into a cell," when referring to an iRNA, means facilitating or effecting uptake or absorption into the cell, as is understood by those skilled in the art. Absorption or uptake of an iRNA can occur through unaided diffusive or active cellular processes, or by auxiliary agents or devices. The meaning of this term is not limited to cells in vitro; an iRNA can also be "introduced into a cell," wherein the cell is part of a living organism. In such an instance, introduction into the cell will include the delivery to the organism. For example, for in vivo delivery, iRNA can be injected into a tissue site or administered systemically. In vivo delivery can also be by a beta-glucan delivery system, such as those described in U.S. Pat. Nos. 5,032,401 and 5,607,677, and U.S. Publication No. 2005/0281781 which are hereby incorporated by reference in their entirety. In vitro introduction into a cell includes methods known in the art such as electroporation and lipofection. Further approaches are described herein below or are known in the art.

As used herein, the term "modulate the expression of," refers to at an least partial "inhibition" or partial "activation" of Mylip/Idol gene expression in a cell treated with an iRNA composition as described herein compared to the expression of Mylip/Idol in an untreated cell.

The terms "activate," "enhance," "up-regulate the expression of," "increase the expression of," and the like, in so far as they refer to a Mylip/Idol gene, herein refer to the at least partial activation of the expression of a Mylip/Idol gene, as manifested by an increase in the amount of Mylip/Idol mRNA, which can be isolated from or detected in a first cell or group of cells in which a Mylip/Idol gene is transcribed and which has or have been treated such that the expression of a Mylip/Idol gene is increased, as compared to a second cell or group of cells substantially identical to the first cell or group of cells but which has or have not been so treated (control cells).

In one embodiment, expression of a Mylip/Idol gene is activated by at least about 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, or 50% by administration of an iRNA as described herein. In some embodiments, a Mylip/Idol gene is activated by at least about 60%, 70%, or 80% by administration of an iRNA featured in the invention. In some embodiments, expression of a Mylip/Idol gene is activated by at least about 85%, 90%, or 95% or more by administration of an iRNA as described herein. In some embodiments, the Mylip/Idol gene expression is increased by at least 1-fold, at least 2-fold, at least 5-fold, at least 10-fold, at least 50-fold, at least 100-fold, at least 500-fold, at least 1000 fold or more in cells treated with an iRNA as described herein compared to the expression in an untreated cell. Activation of expression by small dsRNAs is described, for example, in Li et al., 2006 *Proc. Natl. Acad. Sci. U.S.A.* 103:17337-42, and in US20070111963 and US2005226848, each of which is incorporated herein by reference.

The terms "silence," "inhibit the expression of," "down-regulate the expression of," "suppress the expression of," and the like, in so far as they refer to a Mylip/Idol gene, herein refer to the at least partial suppression of the expression of a Mylip/Idol gene, as manifested by a reduction of the amount of Mylip/Idol mRNA which can be isolated from or detected in a first cell or group of cells in which a Mylip/Idol gene is transcribed and which has or have been treated such that the expression of a Mylip/Idol gene is inhibited, as compared to a second cell or group of cells substantially identical to the first cell or group of cells but which has or have not been so treated (control cells). The degree of inhibition is usually expressed in terms of

$$\frac{(mRNA \text{ in control cells}) - (mRNA \text{ in treated cells})}{(mRNA \text{ in control cells})} \cdot 100\%$$

Alternatively, the degree of inhibition can be given in terms of a reduction of a parameter that is functionally linked to Mylip/Idol gene expression, e.g., the amount of protein encoded by a Mylip/Idol gene, or the number of cells displaying a certain phenotype, e.g., stabilization of microtubules. In principle, Mylip/Idol gene silencing can be determined in any cell expressing Mylip/Idol, either constitutively or by genomic engineering, and by any appropriate assay. However, when a reference is needed in order to determine whether a given iRNA inhibits the expression of the Mylip/Idol gene by a certain degree and therefore is encompassed by the instant invention, the assays provided in the Examples below shall serve as such reference.

For example, in certain instances, expression of a Mylip/Idol gene is suppressed by at least about 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, or 50% by administration of an iRNA featured in the invention. In some embodiments, a Mylip/Idol gene is suppressed by at least about 60%, 70%, or 80% by administration of an iRNA described herein. In some embodiments, a Mylip/Idol gene is suppressed by at least about 85%, 90%, 95%, 98%, 99%, or more, by administration of an iRNA as described herein.

As used herein in the context of Mylip/Idol expression, the terms "treat," "treatment," and the like, refer to relief from or alleviation of pathological processes mediated by Mylip/Idol expression. In the context of the present invention insofar as it relates to any of the other conditions recited herein below (other than pathological processes mediated by Mylip/Idol expression), the terms "treat," "treatment," and the like mean to relieve or alleviate at least one symptom associated with such condition, or to slow or reverse the progression or anticipated progression of such condition, such as slowing the progression of a lipid disorder, such as atherosclerosis.

By "lower" in the context of a disease marker or symptom is meant a statistically significant decrease in such level. The decrease can be, for example, at least 10%, at least 20%, at least 30%, at least 40% or more, and is preferably down to a level accepted as within the range of normal for an individual without such disorder.

As used herein, the phrases "therapeutically effective amount" and "prophylactically effective amount" refer to an amount that provides a therapeutic benefit in the treatment, prevention, or management of pathological processes mediated by Mylip/Idol expression or an overt symptom of pathological processes mediated by Mylip/Idol expression. The specific amount that is therapeutically effective can be readily determined by an ordinary medical practitioner, and can vary depending on factors known in the art, such as, for example, the type of pathological processes mediated by Mylip/Idol expression, the patient's history and age, the stage of pathological processes mediated by Mylip/Idol expression, and the

administration of other agents that inhibit pathological processes mediated by Mylip/Idol expression.

As used herein, a "pharmaceutical composition" comprises a pharmacologically effective amount of an iRNA and a pharmaceutically acceptable carrier. As used herein, "pharmacologically effective amount," "therapeutically effective amount" or simply "effective amount" refers to that amount of an iRNA effective to produce the intended pharmacological, therapeutic or preventive result. For example, if a given clinical treatment is considered effective when there is at least a 10% reduction in a measurable parameter associated with a disease or disorder, a therapeutically effective amount of a drug for the treatment of that disease or disorder is the amount necessary to effect at least a 10% reduction in that parameter. For example, a therapeutically effective amount of an iRNA targeting Mylip/Idol can reduce Mylip/Idol protein levels by at least 10%.

As used herein, the term "neurodegenerative disease" refers to a disorder of the central nervous system including e.g.: intracerebral hemorrhage (ICH), neurodegenerative diseases such as Alzheimer's disease, Parkinson's disease and other degenerative diseases of the basal ganglia; other neurological causes of memory loss or impairment, including Down's syndrome, Creutzfeldt-Jakob disease, prion diseases, cerebral ischemia and stroke; multiple sclerosis; motor neuron disease, such as amyotropic lateral sclerosis; neurological viral disease; Huntington's disease; hereditary spastic hemiplegia; primary lateral sclerosis; spinal muscular atrophy; Kennedy's disease; Shy-Drager syndrome; Progressive Supranuclear Palsy; Lewy Body Disease; neuronopathies; dementia; frontotemporal lobe dementia; affective disorders (e.g. stress, depression and post-traumatic depression); neuropsychiatric disorders (e.g. schizophrenia, multiple sclerosis, and epilepsy); learning and memory disorders; and ocular neuron disorders) trigeminal neuralgia; glossopharyngeal neuralgia; Bell's Palsy; myasthenia gravis; progressive muscular atrophy; progressive bulbar inherited muscular atrophy; herniated, cervical spondylosis; plexus disorders; thoracic outlet destruction syndromes; peripheral neuropathies; prophyria; muscular dystrophy; a polyglutamine repeat disease; and spongiform encephalopathy. In one embodiment, the neurodegenerative disease is a result of injury or trauma and includes e.g., post-surgical neurological dysfunction; ischemic disorders (e.g. cerebral or spinal cord infarction and ischemia, chronic ischemic brain disease, and stroke); kaumas (e.g. caused by physical injury or surgery, and compression injuries); ruptured and prolapsed invertebrate disk syndromes, among others. Ocular neuron disorders can also be treated with the methods and compositions described herein and include, but are not limited to, retina or optic nerve disorders; optic nerve damage and optic neuropathies such as Lebers hereditary optic neuropathy, autosomal dominant optic atrophy, optic neuritis; disorders of the optic nerve or visual pathways; toxic neuropathies and toxic retinopathies; optic atrophy; glaucoma; retinal degenerations such as retinitis pigmentosa, macular degeneration, diabetic retinopathy.

The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent. Such carriers include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The term specifically excludes cell culture medium. For drugs administered orally, pharmaceutically acceptable carriers include, but are not limited to pharmaceutically acceptable excipients such as inert diluents, disintegrating agents, binding agents, lubricating agents, sweetening agents, flavoring agents, coloring agents and preservatives. Suitable inert diluents include sodium and calcium carbonate, sodium and calcium phosphate, and lactose, while corn starch and alginic acid are suitable disintegrating agents. Binding agents may include starch and gelatin, while the lubricating agent, if present, will generally be magnesium stearate, stearic acid or talc. If desired, the tablets may be coated with a material such as glyceryl monostearate or glyceryl distearate, to delay absorption in the gastrointestinal tract. Agents included in drug formulations are described further herein below.

As used herein, a "subject" is a mammal, e.g. a dog, horse, cat, and other non-human primates. In a preferred embodiment, a subject is a human.

As used herein, the term "LNPXX", wherein the "XX" are numerals, is also referred to as "AFXX" herein. For example, LNP09 is also referred to AF09 and LNP12 is also known as or referred to as AF12.

As used herein, the term "comprising" or "comprises" is used in reference to compositions, methods, and respective component(s) thereof, that are essential to the invention, yet open to the inclusion of unspecified elements, whether essential or not.

As used herein, the term "consisting essentially of" refers to those elements required for a given embodiment. The term permits the presence of elements that do not materially affect the basic and novel or functional characteristic(s) of that embodiment of the invention.

The term "consisting of" refers to compositions, methods, and respective components thereof as described herein, which are exclusive of any element not recited in that description of the embodiment.

II. Double-stranded Ribonucleic Acid (dsRNA)

Described herein are iRNA agents that modulate the expression of the Mylip/Idol gene. In one embodiment, the iRNA agent includes double-stranded ribonucleic acid (dsRNA) molecules for inhibiting the expression of a Mylip/Idol gene in a cell or mammal, e.g., in a human having a lipid disorder, where the dsRNA includes an antisense strand having a region of complementarity which is complementary to at least a part of an mRNA formed in the expression of a Mylip/Idol gene, and where the region of complementarity is 30 nucleotides or less in length, generally 19-24 nucleotides in length, and where the dsRNA, upon contact with a cell expressing the Mylip/Idol gene, inhibits the expression of the Mylip/Idol gene by at least 10% as assayed by, for example, a PCR or branched DNA (bDNA)-based method, or by a protein-based method, such as by Western blot. In one embodiment, the iRNA agent activates the expression of a Mylip/Idol gene in a cell or mammal. Expression of a Mylip/Idol gene in cell culture, such as in COS cells, HeLa cells, primary hepatocytes, HepG2 cells, primary cultured cells or in a biological sample from a subject, can be assayed by measuring Mylip/Idol mRNA levels, such as by bDNA or TaqMan assay, or by measuring protein levels, such as by immunofluorescence analysis, using, for example, Western blotting or flow cytometric techniques.

A dsRNA includes two RNA strands that are complementary to hybridize to form a duplex structure under conditions in which the dsRNA will be used. One strand of a dsRNA (the antisense strand) includes a region of complementarity that is substantially complementary, and generally fully complementary, to a target sequence. The target sequence can be derived from the sequence of an mRNA formed during the expression of a Mylip/Idol gene. The other strand (the sense strand) includes a region that is complementary to the antisense strand, such that the two strands hybridize and form a duplex structure when combined under suitable conditions. Generally, the duplex structure is between 15 and 30 inclusive, more generally between 18 and 25 inclusive, yet more

generally between 19 and 24 inclusive, and most generally between 19 and 21 base pairs in length, inclusive. Similarly, the region of complementarity to the target sequence is between 15 and 30 inclusive, more generally between 18 and 25 inclusive, yet more generally between 19 and 24 inclusive, and most generally between 19 and 21 nucleotides in length, inclusive. In some embodiments, the dsRNA is between 15 and 20 nucleotides in length, inclusive, and in other embodiments, the dsRNA is between 25 and 30 nucleotides in length, inclusive. As the ordinarily skilled person will recognize, the targeted region of an RNA targeted for cleavage will most often be part of a larger RNA molecule, often an mRNA molecule. Where relevant, a "part" of an mRNA target is a contiguous sequence of an mRNA target of sufficient length to be a substrate for RNAi-directed cleavage (i.e., cleavage through a RISC pathway). dsRNAs having duplexes as short as 9 base pairs can, under some circumstances, mediate RNAi-directed RNA cleavage. Most often a target will be at least 15 nucleotides in length, preferably 15-30 nucleotides in length.

One of skill in the art will also recognize that the duplex region is a primary functional portion of a dsRNA, e.g., a duplex region of 9 to 36, e.g., 15-30 base pairs. Thus, in one embodiment, to the extent that it becomes processed to a functional duplex of e.g., 15-30 base pairs that targets a desired RNA for cleavage, an RNA molecule or complex of RNA molecules having a duplex region greater than 30 base pairs is a dsRNA. Thus, an ordinarily skilled artisan will recognize that in one embodiment, then, an miRNA is a dsRNA. In another embodiment, a dsRNA is not a naturally occurring miRNA. In another embodiment, an iRNA agent useful to target Mylip/Idol expression is not generated in the target cell by cleavage of a larger dsRNA.

A dsRNA as described herein can further include one or more single-stranded nucleotide overhangs. The dsRNA can be synthesized by standard methods known in the art as further discussed below, e.g., by use of an automated DNA synthesizer, such as are commercially available from, for example, Biosearch, Applied Biosystems, Inc. In one embodiment, a Mylip/Idol gene is a human Mylip/Idol gene. In another embodiment the Mylip/Idol gene is a mouser or a rat Mylip/Idol gene. In specific embodiments, the first sequence is a sense strand of a dsRNA that includes a sense sequence of one of Tables 3 and 5, and the second sequence is selected from the group consisting of the antisense sequences of one of Tables 3 and 5. Alternative dsRNA agents that target elsewhere in the target sequence provided in Tables 3 and 5 can readily be determined using the target sequence and the flanking Mylip/Idol sequence.

In one aspect, a dsRNA will include at least two nucleotide sequences, a sense and an antisense sequence, whereby the sense strand is selected from the groups of sequences provided in Table 3 (SEQ ID NO: 20-SEQ ID NO: 167; SEQ ID NO: 648-SEQ ID NO: 1103), Table 4 (SEQ ID NO: 168-SEQ ID NO: 299), Table 5 (SEQ ID NO: 300-SEQ ID NO: 447), and Table 6 (SEQ ID NO: 448-SEQ ID NO: 579), and the corresponding antisense strand of the sense strand selected from Table 3 (SEQ ID NO: 20-SEQ ID NO: 167; SEQ ID NO: 648-SEQ ID NO: 1103), Table 4 (SEQ ID NO: 168-SEQ ID NO: 299), Table 5 (SEQ ID NO: 300-SEQ ID NO: 447), and Table 6 (SEQ ID NO: 448-SEQ ID NO: 579). In this aspect, one of the two sequences is complementary to the other of the two sequences, with one of the sequences being substantially complementary to a sequence of an mRNA generated in the expression of a Mylip/Idol gene. As such, in this aspect, a dsRNA will include two oligonucleotides, where one oligonucleotide is described as the sense strand in Tables 3, 4, 5 and 6, and the second oligonucleotide is described as the corresponding antisense strand of the sense strand from Tables 3, 4, 5 and 6. As described elsewhere herein and as known in the art, the complementary sequences of a dsRNA can also be contained as self-complementary regions of a single nucleic acid molecule, as opposed to being on separate oligonucleotides.

The skilled person is well aware that dsRNAs having a duplex structure of between 20 and 23, but specifically 21, base pairs have been hailed as particularly effective in inducing RNA interference (Elbashir et al., EMBO 2001, 20:6877-6888). However, others have found that shorter or longer RNA duplex structures can be effective as well. In the embodiments described above, by virtue of the nature of the oligonucleotide sequences provided in Tables 3, 4, 5 and 6, dsRNAs described herein can include at least one strand of a length of minimally 21 nt. It can be reasonably expected that shorter duplexes having one of the sequences of Tables 3, 4, 5 and 6 minus only a few nucleotides on one or both ends may be similarly effective as compared to the dsRNAs described above. Hence, dsRNAs having a partial sequence of at least 15, 16, 17, 18, 19, 20, or more contiguous nucleotides from one of the sequences of Tables 3, 4, 5 and 6, and differing in their ability to inhibit the expression of a Mylip/Idol gene by not more than 5, 10, 15, 20, 25, or 30% inhibition from a dsRNA comprising the full sequence, are contemplated according to the invention.

In addition, the RNAs provided in Tables 3, 4, 5 and 6 identify a site in a Mylip/Idol transcript that is susceptible to RISC-mediated cleavage. As such, the present invention further features iRNAs that target within one of such sequences. As used herein, an iRNA is said to target within a particular site of an RNA transcript if the iRNA promotes cleavage of the transcript anywhere within that particular site. Such an iRNA will generally include at least 15 contiguous nucleotides from one of the sequences provided in Tables 3, 4, 5 and 6 coupled to additional nucleotide sequences taken from the region contiguous to the selected sequence in a Mylip/Idol gene.

While a target sequence is generally 15-30 nucleotides in length, there is wide variation in the suitability of particular sequences in this range for directing cleavage of any given target RNA. Various software packages and the guidelines set out herein provide guidance for the identification of optimal target sequences for any given gene target, but an empirical approach can also be taken in which a "window" or "mask" of a given size (as a non-limiting example, 21 nucleotides) is literally or figuratively (including, e.g., in silico) placed on the target RNA sequence to identify sequences in the size range that may serve as target sequences. By moving the sequence "window" progressively one nucleotide upstream or downstream of an initial target sequence location, the next potential target sequence can be identified, until the complete set of possible sequences is identified for any given target size selected. This process, coupled with systematic synthesis and testing of the identified sequences (using assays as described herein or as known in the art) to identify those sequences that perform optimally can identify those RNA sequences that, when targeted with an iRNA agent, mediate the best inhibition of target gene expression. Thus, while the sequences identified, for example, in Tables 3, 4, 5 and 6 represent effective target sequences, it is contemplated that further optimization of inhibition efficiency can be achieved by progressively "walking the window" one nucleotide upstream or downstream of the given sequences to identify sequences with equal or better inhibition characteristics.

Further, it is contemplated that for any sequence identified, e.g., in Tables 3, 4, 5 and 6, further optimization could be achieved by systematically either adding or removing nucleotides to generate longer or shorter sequences and testing those and sequences generated by walking a window of the longer or shorter size up or down the target RNA from that point. Again, coupling this approach to generating new candidate targets with testing for effectiveness of iRNAs based on those target sequences in an inhibition assay as known in the art or as described herein can lead to further improvements in the efficiency of inhibition. Further still, such optimized sequences can be adjusted by, e.g., the introduction of modified nucleotides as described herein or as known in the art, addition or changes in overhang, or other modifications as known in the art and/or discussed herein to further optimize the molecule (e.g., increasing serum stability or circulating half-life, increasing thermal stability, enhancing transmembrane delivery, targeting to a particular location or cell type, increasing interaction with silencing pathway enzymes, increasing release from endosomes, etc.) as an expression inhibitor.

An iRNA as described herein can contain one or more mismatches to the target sequence. In one embodiment, an iRNA as described herein contains no more than 3 mismatches. If the antisense strand of the iRNA contains mismatches to a target sequence, it is preferable that the area of mismatch not be located in the center of the region of complementarity. If the antisense strand of the iRNA contains mismatches to the target sequence, it is preferable that the mismatch be restricted to be within the last 5 nucleotides from either the 5' or 3' end of the region of complementarity. For example, for a 23 nucleotide iRNA agent RNA strand which is complementary to a region of a Mylip/Idol gene, the RNA strand generally does not contain any mismatch within the central 13 nucleotides. The methods described herein or methods known in the art can be used to determine whether an iRNA containing a mismatch to a target sequence is effective in inhibiting the expression of a Mylip/Idol gene. Consideration of the efficacy of iRNAs with mismatches in inhibiting expression of a Mylip/Idol gene is important, especially if the particular region of complementarity in a Mylip/Idol gene is known to have polymorphic sequence variation within the population.

In one embodiment, at least one end of a dsRNA has a single-stranded nucleotide overhang of 1 to 4, generally 1 or 2 nucleotides. Such dsRNAs having at least one nucleotide overhang have unexpectedly superior inhibitory properties relative to their blunt-ended counterparts. In yet another embodiment, the RNA of an iRNA, e.g., a dsRNA, is chemically modified to enhance stability or other beneficial characteristics. The nucleic acids featured in the invention may be synthesized and/or modified by methods well established in the art, such as those described in "Current protocols in nucleic acid chemistry," Beaucage, S. L. et al. (Edrs.), John Wiley & Sons, Inc., New York, N.Y., USA, which is hereby incorporated herein by reference. Modifications include, for example, (a) end modifications, e.g., 5' end modifications (phosphorylation, conjugation, inverted linkages, etc.) 3' end modifications (conjugation, DNA nucleotides, inverted linkages, etc.), (b) base modifications, e.g., replacement with stabilizing bases, destabilizing bases, or bases that base pair with an expanded repertoire of partners, removal of bases (abasic nucleotides), or conjugated bases, (c) sugar modifications (e.g., at the 2' position or 4' position) or replacement of the sugar, as well as (d) backbone modifications, including modification or replacement of the phosphodiester linkages. Specific examples of RNA compounds useful in the embodiments described herein include, but are not limited to, RNAs containing modified backbones or no natural internucleoside linkages. RNAs having modified backbones include, among others, those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified RNAs that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides. In particular embodiments, the modified RNA will have a phosphorus atom in its internucleoside backbone.

Modified RNA backbones include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those) having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms are also included.

Representative U.S. patents that teach the preparation of the above phosphorus-containing linkages include, but are not limited to, U.S. Pat. Nos. 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,195; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,316; 5,550,111; 5,563,253; 5,571,799; 5,587,361; 5,625,050; 6,028,188; 6,124,445; 6,160,109; 6,169,170; 6,172,209; 6,239,265; 6,277,603; 6,326,199; 6,346,614; 6,444,423; 6,531,590; 6,534,639; 6,608,035; 6,683,167; 6,858,715; 6,867,294; 6,878,805; 7,015,315; 7,041,816; 7,273,933; 7,321,029; and U.S. Pat. RE39464, each of which is herein incorporated by reference.

Modified RNA backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatoms and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH_2 component parts.

Representative U.S. patents that teach the preparation of the above oligonucleosides include, but are not limited to, U.S. Pat. Nos. 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,64,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; and, 5,677,439, each of which is herein incorporated by reference.

In other RNA mimetics suitable or contemplated for use in iRNAs, both the sugar and the internucleoside linkage, i.e., the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an RNA mimetic that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar backbone of an RNA is replaced with an amide containing

backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative U.S. patents that teach the preparation of PNA compounds include, but are not limited to, U.S. Pat. Nos. 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference. Further teaching of PNA compounds can be found, for example, in Nielsen et al., Science, 1991, 254, 1497-1500.

Some embodiments featured in the invention include RNAs with phosphorothioate backbones and oligonucleosides with heteroatom backbones, and in particular —CH_2—NH—CH_2—, —CH_2—N(CH_3)—O—CH_2—[known as a methylene (methylimino) or MMI backbone], —CH_2—O—N(CH_3)—CH_2—, —CH_2—N(CH_3)—N(CH_3)—CH_2— and —N(CH_3)—CH_2—CH_2—[wherein the native phosphodiester backbone is represented as —O—P—O—CH_2—] of the above-referenced U.S. Pat. No. 5,489,677, and the amide backbones of the above-referenced U.S. Pat. No. 5,602,240. In some embodiments, the RNAs featured herein have morpholino backbone structures of the above-referenced U.S. Pat. No. 5,034,506.

Modified RNAs can also contain one or more substituted sugar moieties. The iRNAs, e.g., dsRNAs, featured herein can include one of the following at the 2' position: OH; F; O—, S—, or N-alkyl; O—, S—, or N-alkenyl; O—, S— or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Exemplary suitable modifications include $O[(CH_2)_nO]_mCH_3$, $O(CH_2)_nOCH_3$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nONH_2$, and $O(CH_2)_nON[(CH_2)_nCH_3)]_2$, where n and m are from 1 to about 10. In other embodiments, dsRNAs include one of the following at the 2' position: C_1 to C_{10} lower alkyl, substituted lower alkyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH_3, OCN, Cl, Br, CN, CF_3, OCF_3, $SOCH_3$, SO_2CH_3, ONO_2, NO_2, N_3, NH_2, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an iRNA, or a group for improving the pharmacodynamic properties of an iRNA, and other substituents having similar properties. In some embodiments, the modification includes a 2'-methoxyethoxy (2'-O—$CH_2CH_2OCH_3$, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin et al., *Helv. Chim. Acta,* 1995, 78:486-504) i.e., an alkoxy-alkoxy group. Another exemplary modification is 2'-dimethylaminooxyethoxy, i.e., a $O(CH_2)_2ON(CH_3)_2$ group, also known as 2'-DMAOE, as described in examples herein below, and 2'-dimethylaminoethoxyethoxy (also known in the art as 2'-O-dimethylaminoethoxyethyl or 2'-DMAEOE), i.e., 2'-O—CH_2—O—CH_2—N(CH_2)$_2$, also described in examples herein below.

Other modifications include 2'-methoxy (2'-OCH_3), 2'-aminopropoxy (2'-$OCH_2CH_2CH_2NH_2$) and 2'-fluoro (2'-F). Similar modifications can also be made at other positions on the RNA of an iRNA, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked dsRNAs and the 5' position of 5' terminal nucleotide. iRNAs may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative U.S. patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S. Pat. Nos. 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; and 5,700,920, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference.

An iRNA can also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl anal other 8-substituted adenines and guanines, 5-halo, particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-daazaadenine and 3-deazaguanine and 3-deazaadenine. Further nucleobases include those disclosed in U.S. Pat. No. 3,687, 808, those disclosed in Modified Nucleosides in Biochemistry, Biotechnology and Medicine, Herdewijn, P. ed. Wiley-VCH, 2008; those disclosed in The Concise Encyclopedia Of Polymer Science And Engineering, pages 858-859, Kroschwitz, J. L, ed. John Wiley & Sons, 1990, these disclosed by Englisch et al., Angewandte Chemie, International Edition, 1991, 30, 613, and those disclosed by Sanghvi, Y S., Chapter 15, dsRNA Research and Applications, pages 289-302, Crooke, S. T. and Lebleu, B., Ed., CRC Press, 1993. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds featured in the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and 0-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2° C. (Sanghvi, Y. S., Crooke, S. T. and Lebleu, B., Eds., dsRNA Research and Applications, CRC Press, Boca Raton, 1993, pp. 276-278) and are exemplary base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

Representative U.S. patents that teach the preparation of certain of the above noted modified nucleobases as well as other modified nucleobases include, but are not limited to, the above noted U.S. Pat. No. 3,687,808, as well as U.S. Pat. Nos. 4,845,205; 5,130,30; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; 5,681,941; 6,015,886; 6,147,200; 6,166,197; 6,222,025; 6,235,887; 6,380,368; 6,528,640; 6,639,062; 6,617,438; 7,045,610; 7,427,672; and 7,495,088, each of which is herein incorporated by reference, and U.S. Pat. No. 5,750,692, also herein incorporated by reference.

The RNA of an iRNA can also be modified to include one or more locked nucleic acids (LNA). A locked nucleic acid is a nucleotide having a modified ribose moiety in which the ribose moiety comprises an extra bridge connecting the 2' and 4' carbons. This structure effectively "locks" the ribose in the 3'-endo structural conformation. The addition of locked nucleic acids to siRNAs has been shown to increase siRNA stability in serum, and to reduce off-target effects (Elmen, J. et al., (2005) *Nucleic Acids Research* 33(1):439-447; Mook, O R. et al., (2007) *Mol Canc Ther* 6(3):833-843; Grunweller, A. et al., (2003) *Nucleic Acids Research* 31(12):3185-3193).

Representative U.S. patents that teach the preparation of locked nucleic acid nucleotides include, but are not limited to, the following: U.S. Pat. Nos. 6,268,490; 6,670,461; 6,794,499; 6,998,484; 7,053,207; 7,084,125; and 7,399,845, each of which is herein incorporated by reference in its entirety.

Another modification of the RNA of an iRNA featured in the invention involves chemically linking to the RNA one or more ligands, moieties or conjugates that enhance the activity, cellular distribution, pharmacokinetic properties, or cellular uptake of the iRNA. Such moieties include but are not limited to lipid moieties such as a cholesterol moiety (Letsinger et al., Proc. Natl. Acid. Sci. USA, 1989, 86: 6553-6556), cholic acid (Manoharan et al., Biorg. Med. Chem. Let., 1994, 4:1053-1060), a thioether, e.g., beryl-5-tritylthiol (Manoharan et al., Ann. N.Y. Acad. Sci., 1992, 660:306-309; Manoharan et al., Biorg. Med. Chem. Let., 1993, 3:2765-2770), a thiocholesterol (Oberhauser et al., Nucl. Acids Res., 1992, 20:533-538), an aliphatic chain, e.g., dodecandiol or undecyl residues (Saison-Behmoaras et al., EMBO J, 1991, 10:1111-1118; Kabanov et al., FEBS Lett., 1990, 259:327-330; Svinarchuk et al., Biochimie, 1993, 75:49-54), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethyl-ammonium 1,2-di-O-hexadecyl-rac-glycero-3-phosphonate (Manoharan et al., Tetrahedron Lett., 1995, 36:3651-3654; Shea et al., Nucl. Acids Res., 1990, 18:3777-3783), a polyamine or a polyethylene glycol chain (Manoharan et al., Nucleosides & Nucleotides, 1995, 14:969-973), or adamantane acetic acid (Manoharan et al., Tetrahedron Lett., 1995, 36:3651-3654), a palmityl moiety (Mishra et al., Biochim. Biophys. Acta, 1995, 1264:229-237), or an octadecylamine or hexylamino-carbonyloxycholesterol moiety (Crooke et al., J. Pharmacol. Exp. Ther., 1996, 277:923-937).

In one embodiment, a ligand alters the distribution, targeting or lifetime of an iRNA agent into which it is incorporated. In preferred embodiments a ligand provides an enhanced affinity for a selected target, e.g., molecule, cell or cell type, compartment, e.g., a cellular or organ compartment, tissue, organ or region of the body, as, e.g., compared to a species absent such a ligand. Preferred ligands will not take part in duplex pairing in a duplexed nucleic acid.

Ligands can include a naturally occurring substance, such as a protein (e.g., human serum albumin (HSA), low-density lipoprotein (LDL), or globulin); carbohydrate (e.g., a dextran, pullulan, chitin, chitosan, inulin, cyclodextrin or hyaluronic acid); or a lipid. The ligand may also be a recombinant or synthetic molecule, such as a synthetic polymer, e.g., a synthetic polyamino acid. Examples of polyamino acids include polyamino acid is a polylysine (PLL), poly L-aspartic acid, poly L-glutamic acid, styrene-maleic acid anhydride copolymer, poly(L-lactide-co-glycolied) copolymer, divinyl ether-maleic anhydride copolymer, N-(2-hydroxypropyl)methacrylamide copolymer (HMPA), polyethylene glycol (PEG), polyvinyl alcohol (PVA), polyurethane, poly(2-ethylacryllic acid), N-isopropylacrylamide polymers, or polyphosphazine. Example of polyamines include: polyethylenimine, polylysine (PLL), spermine, spermidine, polyamine, pseudopeptide-polyamine, peptidomimetic polyamine, dendrimer polyamine, arginine, amidine, protamine, cationic lipid, cationic porphyrin, quaternary salt of a polyamine, or an alpha helical peptide.

Ligands can also include targeting groups, e.g., a cell or tissue targeting agent, e.g., a lectin, glycoprotein, lipid or protein, e.g., an antibody, that binds to a specified cell type such as a kidney cell. A targeting group can be a thyrotropin, melanotropin, lectin, glycoprotein, surfactant protein A, Mucin carbohydrate, multivalent lactose, multivalent galactose, N-acetyl-galactosamine, N-acetyl-gulucosamine multivalent mannose, multivalent fucose, glycosylated polyaminoacids, multivalent galactose, transferrin, bisphosphonate, polyglutamate, polyaspartate, a lipid, cholesterol, a steroid, bile acid, folate, vitamin B12, vitamin A, biotin, or an RGD peptide or RGD peptide mimetic.

Other examples of ligands include dyes, intercalating agents (e.g. acridines), cross-linkers (e.g. psoralene, mitomycin C), porphyrins (TPPC4, texaphyrin, Sapphyrin), polycyclic aromatic hydrocarbons (e.g., phenazine, dihydrophenazine), artificial endonucleases (e.g. EDTA), lipophilic molecules, e.g., cholesterol, cholic acid, adamantane acetic acid, 1-pyrene butyric acid, dihydrotestosterone, 1,3-Bis-O (hexadecyl)glycerol, geranyloxyhexyl group, hexadecylglycerol, borneol, menthol, 1,3-propanediol, heptadecyl group, palmitic acid, myristic acid, O3-(oleoyl)lithocholic acid, O3-(oleoyl)cholenic acid, dimethoxytrityl, or phenoxazine) and peptide conjugates (e.g., antennapedia peptide, Tat peptide), alkylating agents, phosphate, amino, mercapto, PEG (e.g., PEG-40K), MPEG, $[MPEG]_2$, polyamino, alkyl, substituted alkyl, radiolabeled markers, enzymes, haptens (e.g. biotin), transport/absorption facilitators (e.g., aspirin, vitamin E, folic acid), synthetic ribonucleases (e.g., imidazole, bisimidazole, histamine, imidazole clusters, acridine-imidazole conjugates, Eu3+ complexes of tetraazamacrocycles), dinitrophenyl, HRP, or AP.

Ligands can be proteins, e.g., glycoproteins, or peptides, e.g., molecules having a specific affinity for a co-ligand, or antibodies e.g., an antibody, that binds to a specified cell type such as a cancer cell, endothelial cell, or bone cell. Ligands may also include hormones and hormone receptors. They can also include non-peptidic species, such as lipids, lectins, carbohydrates, vitamins, cofactors, multivalent lactose, multivalent galactose, N-acetyl-galactosamine, N-acetyl-gulucosamine multivalent mannose, or multivalent fucose. The ligand can be, for example, a lipopolysaccharide, an activator of p38 MAP kinase, or an activator of NF-κB.

The ligand can be a substance, e.g., a drug, which can increase the uptake of the iRNA agent into the cell, for example, by disrupting the cell's cytoskeleton, e.g., by disrupting the cell's microtubules, microfilaments, and/or intermediate filaments. The drug can be, for example, taxon, vincristine, vinblastine, cytochalasin, nocodazole, japlakinolide, latrunculin A, phalloidin, swinholide A, indanocine, or myoservin.

In some embodiments, a ligand attached to an iRNA as described herein acts as a PK modulator. As used herein, a "PK modulator" refers to a pharmacokinetic modulator. PK modulators include lipophiles, bile acids, steroids, phospholipid analogues, peptides, protein binding agents, PEG, vitamins etc. Examplary PK modulators include, but are not limited to, cholesterol, fatty acids, cholic acid, lithocholic acid, dialkylglycerides, diacylglyceride, phospholipids, sphingolipids, naproxen, ibuprofen, vitamin E, biotin etc. Oligonucleotides that comprise a number of phosphorothioate linkages are also known to bind to serum protein, thus short oligonucleotides, e.g., oligonucleotides of about 5 bases, 10 bases, 15 bases or 20 bases, comprising multiple of phosphorothioate linkages in the backbaone are also amenable to the present invention as ligands (e.g. as PK modulating ligands). In addition, aptamers that bind serum components (e.g. serum proteins) are also suitable for use as PK modulating ligands in the embodiments described herein.

For macromolecular drugs and hydrophilic drug molecules, which cannot easily cross bilayer membranes, entrapment in endosomal/lysosomal compartments of the cell is thought to be the biggest hurdle for effective delivery to their site of action. In recent years, a number of approaches and

strategies have been devised to address this problem. For liposomal formulations, the use of fusogenic lipids in the formulation have been the most common approach (Singh, R. S., Goncalves, C. et al. (2004). On the Gene Delivery Efficacies of pH-Sensitive Cationic Lipids via Endosomal Protonation. A Chemical Biology Investigation. Chem. Biol. 11, 713-723.). Other components, which exhibit pH-sensitive endosomolytic activity through protonation and/or pH-induced conformational changes, include charged polymers and peptides. Examples may be found in Hoffman, A. S., Stayton, P. S. et al. (2002). Design of "smart" polymers that can direct intracellular drug delivery. Polymers Adv. Technol. 13, 992-999; Kakudo, Chaki, T., S. et al. (2004). Transferrin-Modified Liposomes Equipped with a pH-Sensitive Fusogenic Peptide: An Artificial Viral-like Delivery System. Biochemistry 436, 5618-5628; Yessine, M. A. and Leroux, J. C. (2004). Membrane-destabilizing polyanions: interaction with lipid bilayers and endosomal escape of biomacromolecules. Adv. Drug Deliv. Rev. 56, 999-1021; Oliveira, S., van Rooy, I. et al. (2007). Fusogenic peptides enhance endosomal escape improving iRNA-induced silencing of oncogenes. Int. J. Pharm. 331, 211-4. They have generally been used in the context of drug delivery systems, such as liposomes or lipoplexes. For folate receptor-mediated delivery using liposomal formulations, for instance, a pH-sensitive fusogenic peptide has been incorporated into the liposomes and shown to enhance the activity through improving the unloading of drug during the uptake process (Turk, M. J., Reddy, J. A. et al. (2002). Characterization of a novel pH-sensitive peptide that enhances drug release from folate-targeted liposomes at endosomal pHs is described in Biochim. Biophys. Acta 1559, 56-68).

In certain embodiments, the endosomolytic components of the present invention can be polyanionic peptides or peptidomimetics which show pH-dependent membrane activity and/or fusogenicity. A peptidomimetic can be a small protein-like chain designed to mimic a peptide. A peptidomimetic can arise from modification of an existing peptide in order to alter the molecule's properties, or the synthesis of a peptide-like molecule using unnatural amino acids or their analogs. In certain embodiments, they have improved stability and/or biological activity when compared to a peptide. In certain embodiments, the endosomolytic component assumes its active conformation at endosomal pH (e.g., pH 5-6). The "active" conformation is that conformation in which the endosomolytic component promotes lysis of the endosome and/or transport of the modular composition of the invention, or its any of its components (e.g., a nucleic acid), from the endosome to the cytoplasm of the cell.

Libraries of compounds can be screened for their differential membrane activity at endosomal pH versus neutral pH using a hemolysis assay. Promising candidates isolated by this method may be used as components of the modular compositions of the invention. A method for identifying an endosomolytic component for use in the compositions and methods of the present invention may comprise: providing a library of compounds; contacting blood cells with the members of the library, wherein the pH of the medium in which the contact occurs is controlled; determining whether the compounds induce differential lysis of blood cells at a low pH (e.g., about pH 5-6) versus neutral pH (e.g., about pH 7-8).

Exemplary endosomolytic components include the GALA peptide (Subbarao et al., Biochemistry, 1987, 26: 2964-2972), the EALA peptide (Vogel et al., J. Am. Chem. Soc., 1996, 118: 1581-1586), and their derivatives (Turk et al., Biochem. Biophys. Acta, 2002, 1559: 56-68). In certain embodiments, the endosomolytic component can contain a chemical group (e.g., an amino acid) which will undergo a change in charge or protonation in response to a change in pH. The endosomolytic component may be linear or branched. Exemplary primary sequences of endosomolytic components include H2N-(AALEALAEALEALAEALEALAE-AAAAGGC)-CO2H (SEQ ID NO: 1104); H2N-(AALAE-ALAEALAEALAEALAEALAAAAGGC)-CO2H (SEQ ID NO: 1105); and H2N-(ALEALAEALEALAEA)-CONH2 (SEQ ID NO: 1106).

In certain embodiments, more than one endosomolytic component can be incorporated into the iRNA agent of the invention. In some embodiments, this will entail incorporating more than one of the same endosomolytic component into the iRNA agent. In other embodiments, this will entail incorporating two or more different endosomolytic components into iRNA agent.

These endosomolytic components can mediate endosomal escape by, for example, changing conformation at endosomal pH. In certain embodiments, the endosomolytic components can exist in a random coil conformation at neutral pH and rearrange to an amphipathic helix at endosomal pH. As a consequence of this conformational transition, these peptides may insert into the lipid membrane of the endosome, causing leakage of the endosomal contents into the cytoplasm. Because the conformational transition is pH-dependent, the endosomolytic components can display little or no fusogenic activity while circulating in the blood (pH~7.4). "Fusogenic activity," as used herein, is defined as that activity which results in disruption of a lipid membrane by the endosomolytic component. One example of fusogenic activity is the disruption of the endosomal membrane by the endosomolytic component, leading to endosomal lysis or leakage and transport of one or more components of the modular composition of the invention (e.g., the nucleic acid) from the endosome into the cytoplasm.

In addition to hemolysis assays, as described herein, suitable endosomolytic components can be tested and identified by a skilled artisan using other methods. For example, the ability of a compound to respond to, e.g., change charge depending on, the pH environment can be tested by routine methods, e.g., in a cellular assay. In certain embodiments, a test compound is combined with or contacted with a cell, and the cell is allowed to internalize the test compound, e.g., by endocytosis. An endosome preparation can then be made from the contacted cells and the endosome preparation compared to an endosome preparation from control cells. A change, e.g., a decrease, in the endosome fraction from the contacted cell vs. the control cell indicates that the test compound can function as a fusogenic agent. Alternatively, the contacted cell and control cell can be evaluated, e.g., by microscopy, e.g., by light or electron microscopy, to determine a difference in the endosome population in the cells. The test compound and/or the endosomes can labeled, e.g., to quantify endosomal leakage.

In another type of assay, an iRNA agent described herein is constructed using one or more test or putative fusogenic agents. The iRNA agent can be labeled for easy visulization. The ability of the endosomolytic component to promote endosomal escape, once the iRNA agnet is taken up by the cell, can be evaluated, e.g., by preparation of an endosome preparation, or by microscopy techniques, which enable visualization of the labeled iRNA agent in the cytoplasm of the cell. In certain other embodiments, the inhibition of gene expression, or any other physiological parameter, may be used as a surrogate marker for endosomal escape.

In other embodiments, circular dichroism spectroscopy can be used to identify compounds that exhibit a pH-dependent structural transition.

A two-step assay can also be performed, wherein a first assay evaluates the ability of a test compound alone to respond to changes in pH, and a second assay evaluates the ability of a modular composition that includes the test compound to respond to changes in pH.

Lipid Conjugates

In one ligand, the ligand or conjugate is a lipid or lipid-based molecule. Such a lipid or lipid-based molecule preferably binds a serum protein, e.g., human serum albumin (HSA). An HSA binding ligand allows for distribution of the conjugate to a target tissue, e.g., a non-kidney target tissue of the body. For example, the target tissue can be the liver, including parenchymal cells of the liver. Other molecules that can bind HSA can also be used as ligands. For example, neproxin or aspirin can be used. A lipid or lipid-based ligand can (a) increase resistance to degradation of the conjugate, (b) increase targeting or transport into a target cell or cell membrane, and/or (c) can be used to adjust binding to a serum protein, e.g., HSA.

A lipid based ligand can be used to modulate, e.g., control the binding of the conjugate to a target tissue. For example, a lipid or lipid-based ligand that binds to HSA more strongly will be less likely to be targeted to the kidney and therefore less likely to be cleared from the body. A lipid or lipid-based ligand that binds to HSA less strongly can be used to target the conjugate to the kidney.

In a preferred embodiment, the lipid based ligand binds HSA. Preferably, it binds HSA with a sufficient affinity such that the conjugate will be preferably distributed to a non-kidney tissue. However, it is preferred that the affinity not be so strong that the HSA-ligand binding cannot be reversed.

In another preferred embodiment, the lipid based ligand binds HSA weakly or not at all, such that the conjugate will be preferably distributed to the kidney. Other moieties that target to kidney cells can also be used in place of or in addition to the lipid based ligand.

In another aspect, the ligand is a moiety, e.g., a vitamin, which is taken up by a target cell, e.g., a proliferating cell. These are particularly useful for treating disorders characterized by unwanted cell proliferation, e.g., of the malignant or non-malignant type, e.g., cancer cells. Exemplary vitamins include vitamin A, E, and K. Other exemplary vitamins include are B vitamin, e.g., folic acid, B12, riboflavin, biotin, pyridoxal or other vitamins or nutrients taken up by cancer cells. Also included are HSA and low density lipoprotein (LDL).

In another aspect, the ligand is a cell-permeation agent, preferably a helical cell-permeation agent. Preferably, the agent is amphipathic. An exemplary agent is a peptide such as tat or antennopedia. If the agent is a peptide, it can be modified, including a peptidylmimetic, invertomers, non-peptide or pseudo-peptide linkages, and use of D-amino acids. The helical agent is preferably an alpha-helical agent, which preferably has a lipophilic and a lipophobic phase.

Cell Permeation Peptides

Peptides suitable for use with the present invention can be a natural peptide, .e.g., tat or antennopedia peptide, a synthetic peptide, or a peptidomimetic. Furthermore, the peptide can be a modified peptide, for example peptide can comprise non-peptide or pseudo-peptide linkages, and D-amino acids. A peptidomimetic (also referred to herein as an oligopeptidomimetic) is a molecule capable of folding into a defined three-dimensional structure similar to a natural peptide. The attachment of peptide and peptidomimetics to iRNA agents can affect pharmacokinetic distribution of the iRNA, such as by enhancing cellular recognition and absorption. The peptide or peptidomimetic moiety can be about 5-50 amino acids long, e.g., about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 amino acids long.

A peptide or peptidomimetic can be, for example, a cell permeation peptide, cationic peptide, amphipathic peptide, or hydrophobic peptide (e.g., consisting primarily of Tyr, Trp or Phe). The peptide moiety can be a dendrimer peptide, constrained peptide or crosslinked peptide. In another alternative, the peptide moiety can include a hydrophobic membrane translocation sequence (MTS). An exemplary hydrophobic MTS-containing peptide is RFGF having the amino acid sequence AAVALLPAVLLALLAP (SEQ ID NO:16). An RFGF analogue (e.g., amino acid sequence AALLPVLLAAP (SEQ ID NO:17)) containing a hydrophobic MTS can also be a targeting moiety. The peptide moiety can be a "delivery" peptide, which can carry large polar molecules including peptides, oligonucleotides, and protein across cell membranes. For example, sequences from the HIV Tat protein (GRKKRRQRRRPPQ (SEQ ID NO:18)) and the *Drosophila* Antennapedia protein (RQIKIWFQNRRMKWKK (SEQ ID NO:19)) have been found to be capable of functioning as delivery peptides. A peptide or peptidomimetic can be encoded by a random sequence of DNA, such as a peptide identified from a phage-display library, or one-bead-one-compound (OBOC) combinatorial library (Lam et al., Nature, 354:82-84, 1991). Preferably, the peptide or peptidomimetic tethered to the lipid is a cell-targeting peptide such as an arginine-glycine-aspartic acid (RGD)-peptide, or RGD mimic. A peptide moiety can range in length from about 5 amino acids to about 40 amino acids. The peptide moieties can have a structural modification, such as to increase stability or direct conformational properties. Any of the structural modifications described below can be utilized.

An RGD peptide moiety can be used to target a tumor cell, such as an endothelial tumor cell or a breast cancer tumor cell (Zitzmann et al., Cancer Res., 62:5139-43, 2002). An RGD peptide can facilitate targeting of an dsRNA agent to tumors of a variety of other tissues, including the lung, kidney, spleen, or liver (Aoki et al., Cancer Gene Therapy 8:783-787, 2001). Preferably, the RGD peptide will facilitate targeting of an iRNA agent to the kidney. The RGD peptide can be linear or cyclic, and can be modified, e.g., glycosylated or methylated to facilitate targeting to specific tissues. For example, a glycosylated RGD peptide can deliver a iRNA agent to a tumor cell expressing $\alpha_v\beta_3$ (Haubner et al., Jour. Nucl. Med., 42:326-336, 2001).

Peptides that target markers enriched in proliferating cells can be used. E.g., RGD containing peptides and peptidomimetics can target cancer cells, in particular cells that exhibit an αvβ3 integrin. Thus, one could use RGD peptides, cyclic peptides containing RGD, RGD peptides that include D-amino acids, as well as synthetic RGD mimics. In addition to RGD, one can use other moieties that target the αvβ3 integrin ligand. Generally, such ligands can be used to control proliferating cells and angiogeneis.

A "cell permeation peptide" is capable of permeating a cell, e.g., a microbial cell, such as a bacterial or fungal cell, or a mammalian cell, such as a human cell. A microbial cell-permeating peptide can be, for example, an α-helical linear peptide (e.g., LL-37 or Ceropin P1), a disulfide bond-containing peptide (e.g., α-defensin, β-defensin or bactenecin), or a peptide containing only one or two dominating amino acids (e.g., PR-39 or indolicidin). A cell permeation peptide can also include a nuclear localization signal (NLS). For example, a cell permeation peptide can be a bipartite amphipathic pep-

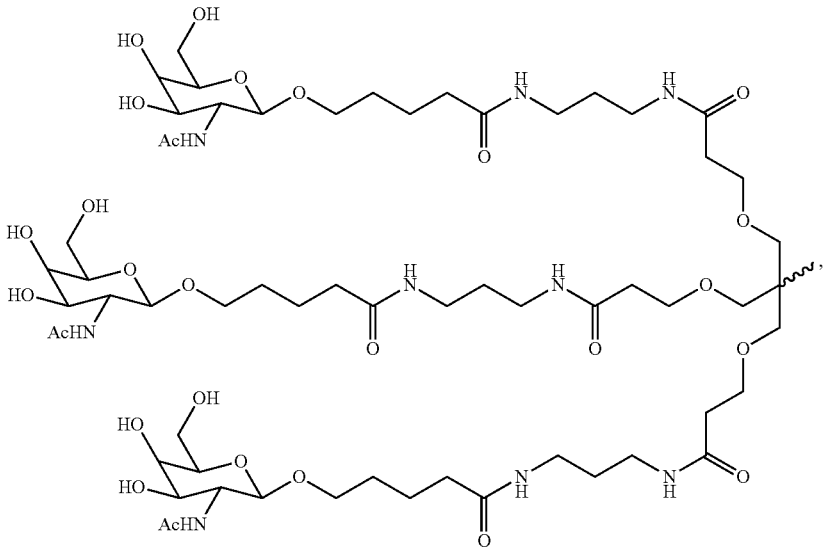
tide, such as MPG, which is derived from the fusion peptide domain of HIV-1 gp41 and the NLS of SV40 large T antigen (Simeoni et al., Nucl. Acids Res. 31:2717-2724, 2003).

Carbohydrate Conjugates

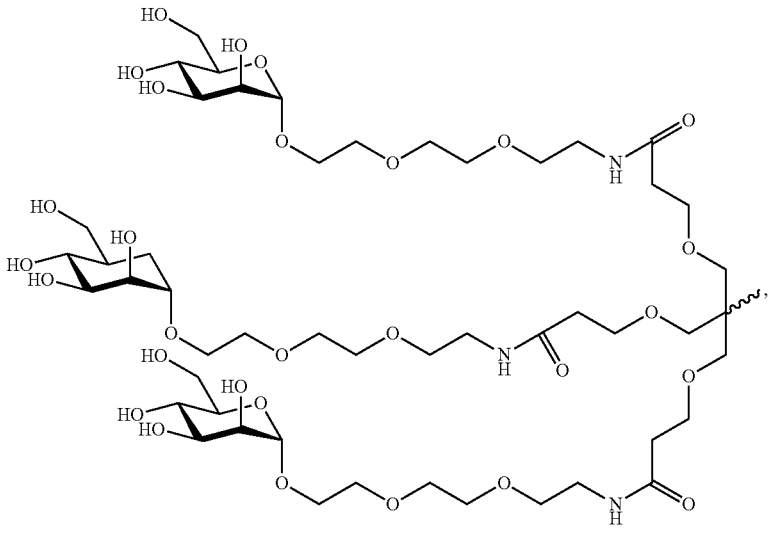
In some embodiments, the iRNA oligonucleotides described herein further comprise carbohydrate conjugates. The carbohydrate conjugates are advantageous for the in vivo delivery of nucleic acids, as well as compositions suitable for in vivo therapeutic use, as described herein. As used herein, "carbohydrate" refers to a compound which is either a carbohydrate per se made up of one or more monosaccharide units having at least 6 carbon atoms (which may be linear, branched or cyclic) with an oxygen, nitrogen or sulfur atom bonded to each carbon atom; or a compound having as a part thereof a carbohydrate moiety made up of one or more monosaccharide units each having at least six carbon atoms (which may be linear, branched or cyclic), with an oxygen, nitrogen or sulfur atom bonded to each carbon atom. Representative carbohydrates include the sugars (mono-, di-, tri- and oligosaccharides containing from about 4-9 monosaccharide units), and polysaccharides such as starches, glycogen, cellulose and polysaccharide gums. Specific monosaccharides include C_5 and above (preferably C_5-C_8) sugars; di- and trisaccharides include sugars having two or three monosaccharide units (preferably C_5-C_8).

In one embodiment, the carbohydrate conjugate is selected from the group consisting of:

Formula II

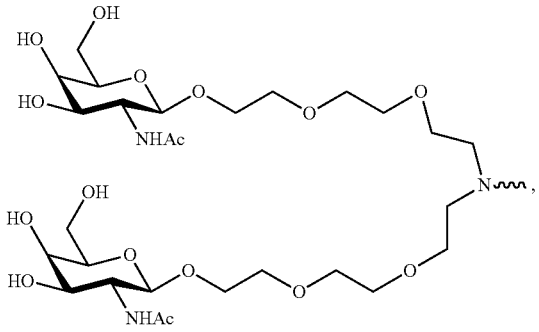


Formula III

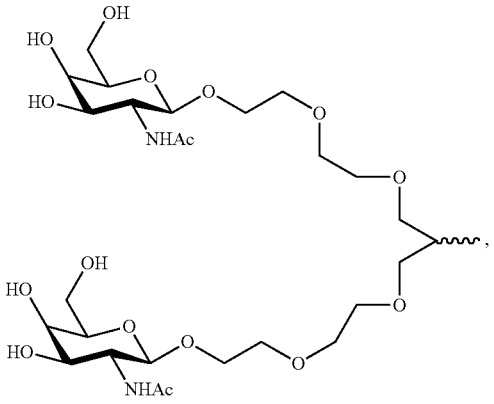


-continued

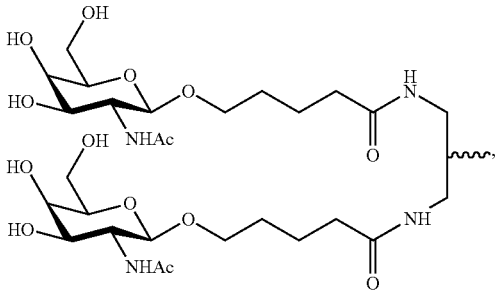
Formula IV



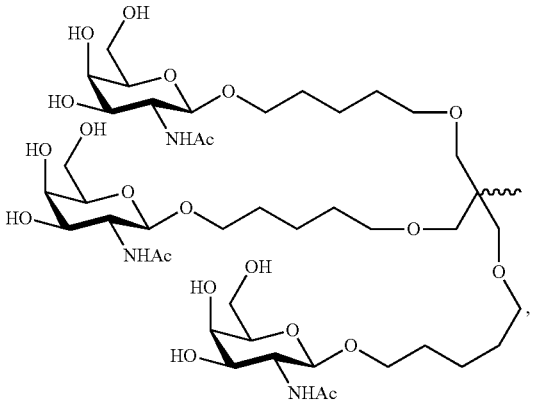
Formula V



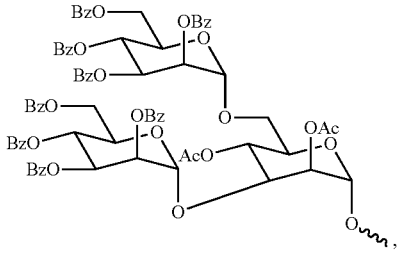
Formula VI



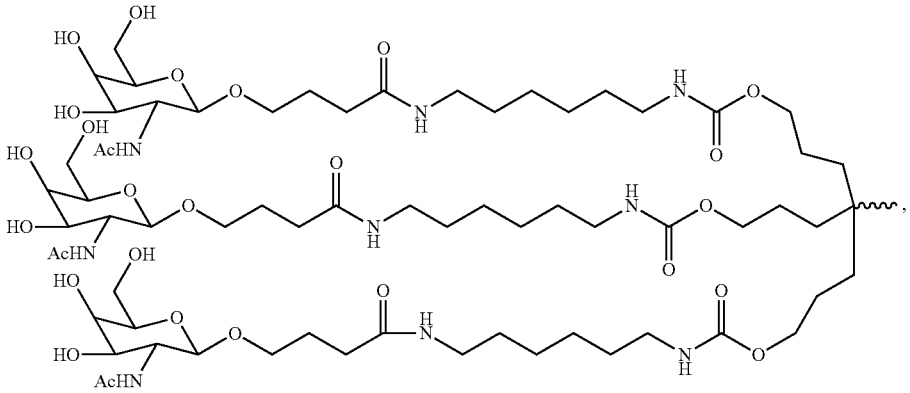
Formula VII



Formula VIII



Formula IX



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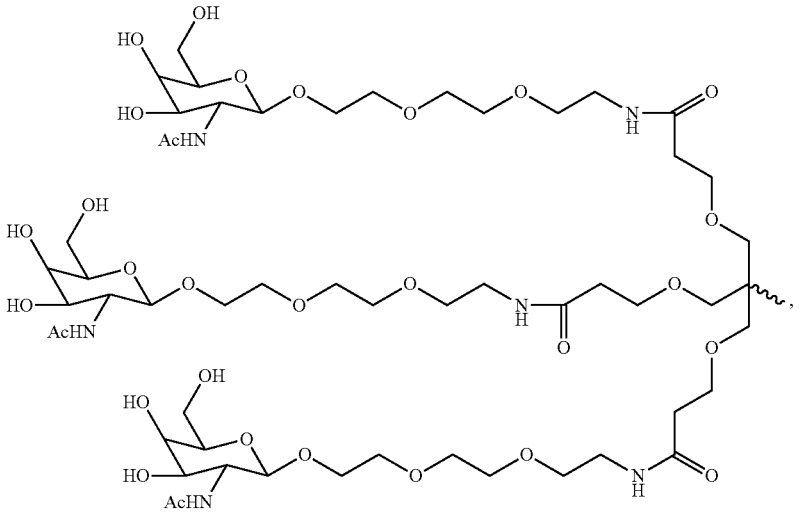
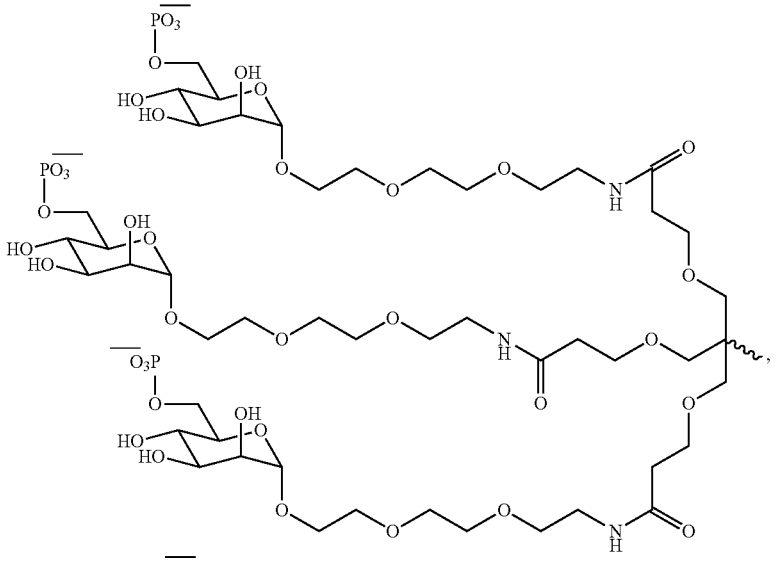
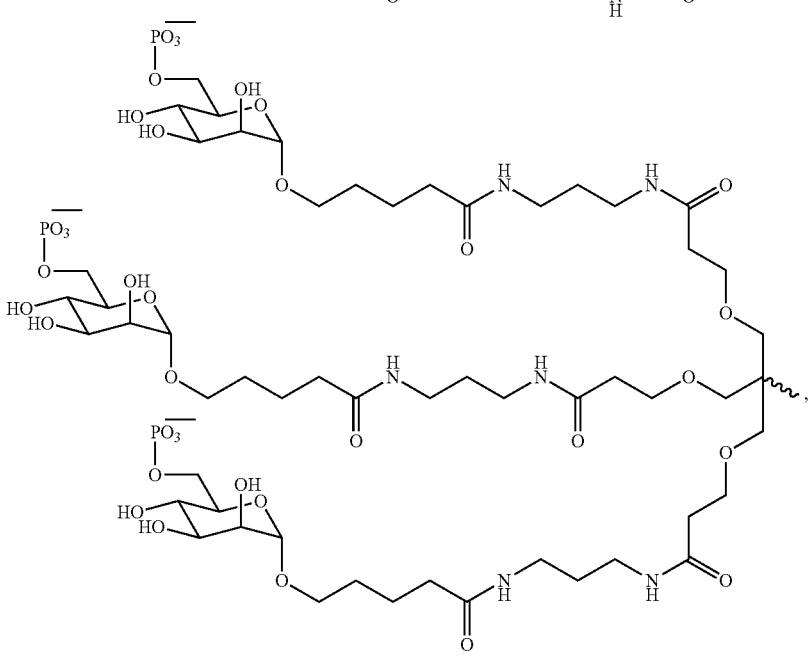
Formula X



Formula XI

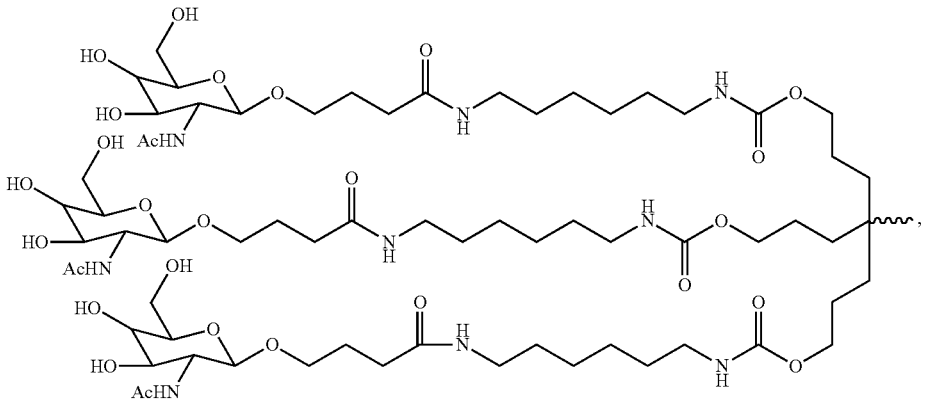


Formula XII

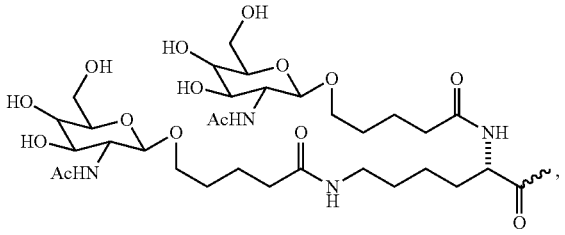


-continued

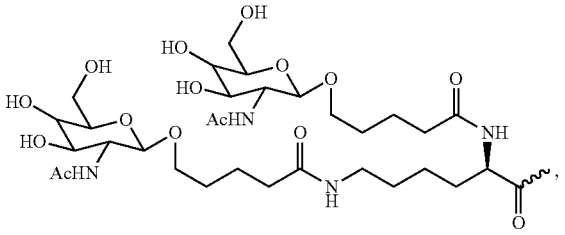
Formula XIII



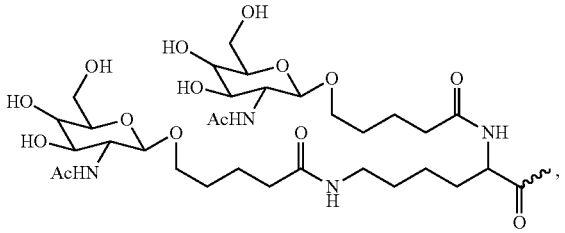
Formula XIV



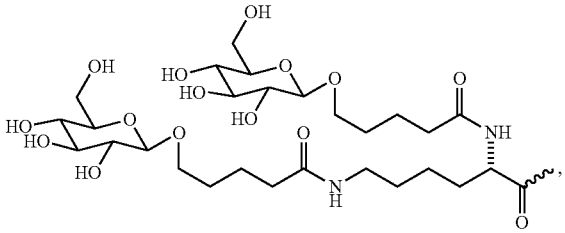
Formula XV



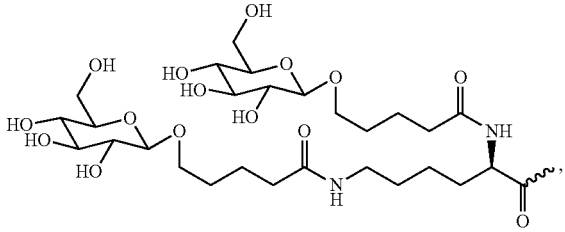
Formula XVI



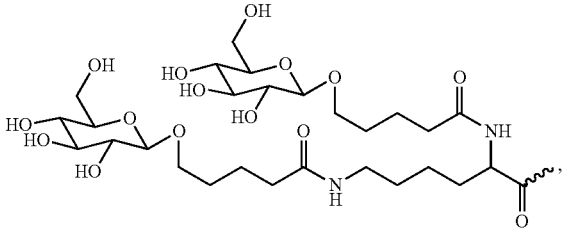
Formula XVII



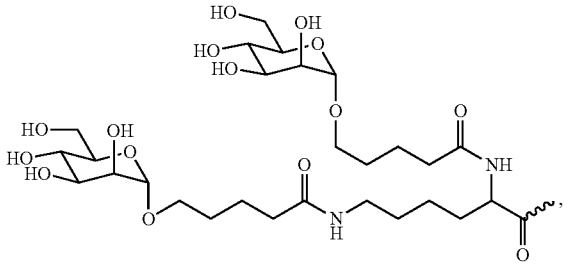
Formula XVIII



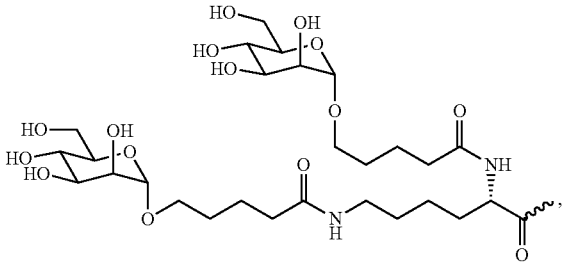
Formula XIX



Formula XX



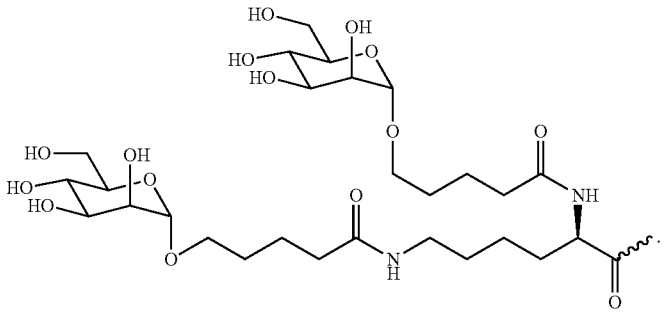
Formula XXI



-continued

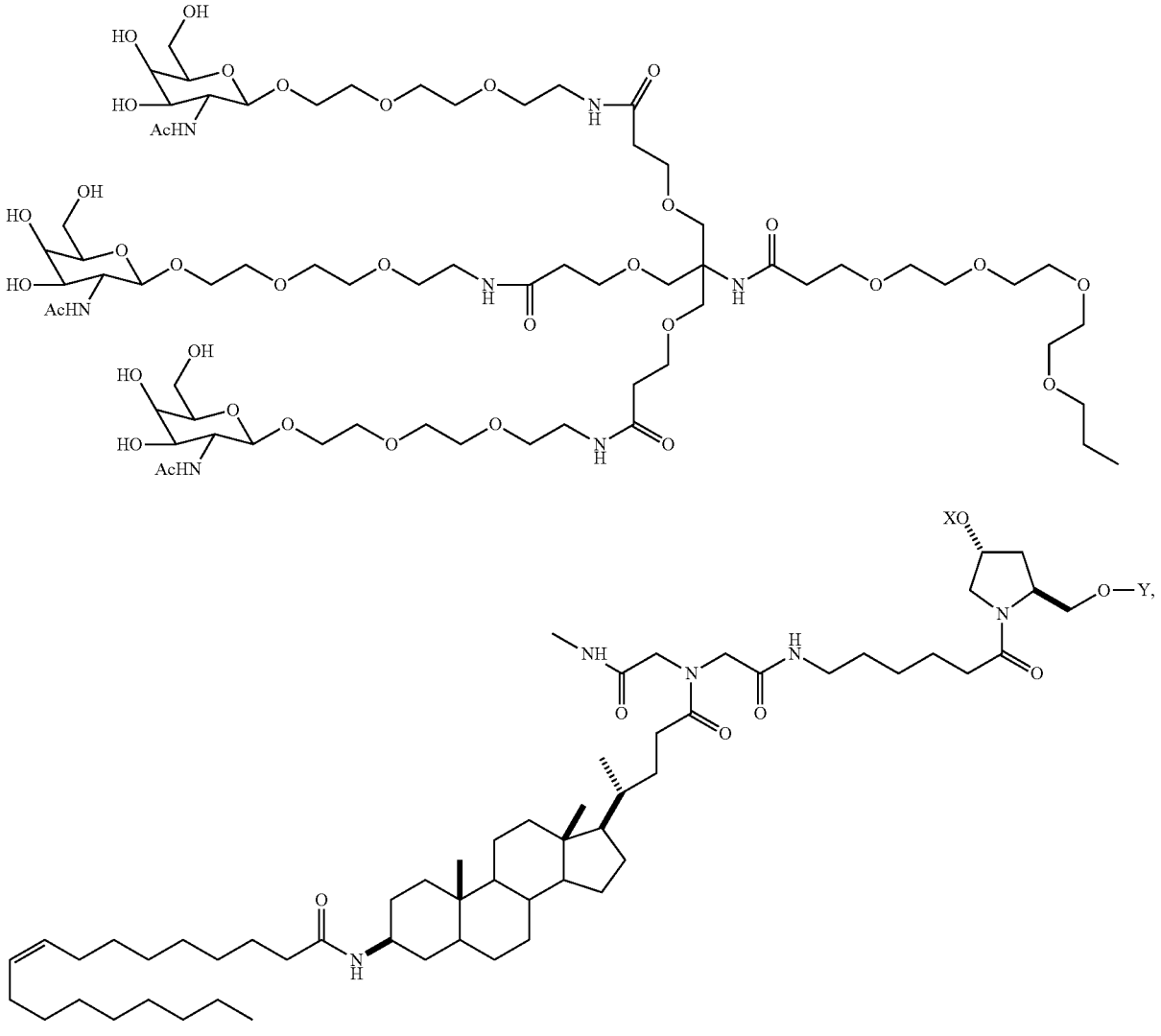
i.e., Formula II-Formula XXII

Formula XXII



Another representative carbohydrate conjugate for use in the embodiments described herein includes, but is not limited to,

(Formula XXIII)



when one of X or Y is an oligonucleotide, the other is a hydrogen.

In some embodiments, the carbohydrate conjugate further comprises other ligand such as, but not limited to, PK modulator, endosomolytic ligand, and cell permeation peptide.

Linkers

In some embodiments, the conjugates described herein can be attached to the iRNA oligonucleotide with various linkers that can be cleavable or non cleavable.

The term "linker" or "linking group" means an organic moiety that connects two parts of a compound. Linkers typically comprise a direct bond or an atom such as oxygen or sulfur, a unit such as NR^8, C(O), C(O)NH, SO, SO_2, SO_2NH or a chain of atoms, such as, but not limited to, substituted or unsubstituted alkyl, substituted or unsubstituted alkenyl, substituted or unsubstituted alkynyl, arylalkyl, arylalkenyl, arylalkynyl, heteroarylalkyl, heteroarylalkenyl, heteroarylalkynyl, heterocyclylalkyl, heterocyclylalkenyl, heterocyclylalkynyl, aryl, heteroaryl, heterocyclyl, cycloalkyl, cycloalkenyl, alkylarylalkyl, alkylarylalkenyl, alkylarylalkynyl, alkenylarylalkyl, alkenylarylalkenyl, alkenylarylalkynyl, alkynylarylalkyl, alkynylarylalkenyl, alkynylarylalkynyl, alkylheteroarylalkyl, alkylheteroarylalkenyl, alkylheteroarylalkynyl, alkenylheteroarylalkyl, alkenylheteroarylalkenyl, alkenylheteroarylalkynyl, alkynylheteroarylalkyl, alkynylheteroarylalkenyl, alkynylheteroarylalkynyl, alkylheterocyclylalkyl, alkylheterocyclylalkenyl, alkylherocyclylalkynyl, alkenylheterocyclylalkyl, alkenylheterocyclylalkenyl, alkenylheterocyclylalkynyl, alkynylheterocyclylalkyl, alkynylheterocyclylalkenyl, alkynylheterocyclylalkynyl, alkylaryl, alkenylaryl, alkynylaryl, alkylheteroaryl, alkenylheteroaryl, alkynylhereroaryl, which one or more methylenes can be interrupted or terminated by O, S, S(O), SO_2, $N(R^8)$, C(O), substituted or unsubstituted aryl, substituted or unsubstituted heteroaryl, substituted or unsubstituted heterocyclic; where R^8 is hydrogen, acyl, aliphatic or substituted aliphatic. In one embodiment, the linker is between 1-24 atoms, preferably 4-24 atoms, preferably 6-18 atoms, more preferably 8-18 atoms, and most preferably 8-16 atoms.

A cleavable linking group is one which is sufficiently stable outside the cell, but which upon entry into a target cell is cleaved to release the two parts the linker is holding together. In a preferred embodiment, the cleavable linking group is cleaved at least 10 times or more, preferably at least 100 times faster in the target cell or under a first reference condition (which can, e.g., be selected to mimic or represent intracellular conditions) than in the blood of a subject, or under a second reference condition (which can, e.g., be selected to mimic or represent conditions found in the blood or serum).

Cleavable linking groups are susceptible to cleavage agents, e.g., pH, redox potential or the presence of degradative molecules. Generally, cleavage agents are more prevalent or found at higher levels or activities inside cells than in serum or blood. Examples of such degradative agents include: redox agents which are selected for particular substrates or which have no substrate specificity, including, e.g., oxidative or reductive enzymes or reductive agents such as mercaptans, present in cells, that can degrade a redox cleavable linking group by reduction; esterases; endosomes or agents that can create an acidic environment, e.g., those that result in a pH of five or lower; enzymes that can hydrolyze or degrade an acid cleavable linking group by acting as a general acid, peptidases (which can be substrate specific), and phosphatases.

A cleavable linkage group, such as a disulfide bond can be susceptible to pH. The pH of human serum is 7.4, while the average intracellular pH is slightly lower, ranging from about 7.1-7.3. Endosomes have a more acidic pH, in the range of 5.5-6.0, and lysosomes have an even more acidic pH at around 5.0. Some linkers will have a cleavable linking group that is cleaved at a preferred pH, thereby releasing the cationic lipid from the ligand inside the cell, or into the desired compartment of the cell.

A linker can include a cleavable linking group that is cleavable by a particular enzyme. The type of cleavable linking group incorporated into a linker can depend on the cell to be targeted. For example, liver targeting ligands can be linked to the cationic lipids through a linker that includes an ester group. Liver cells are rich in esterases, and therefore the linker will be cleaved more efficiently in liver cells than in cell types that are not esterase-rich. Other cell-types rich in esterases include cells of the lung, renal cortex, and testis.

Linkers that contain peptide bonds can be used when targeting cell types rich in peptidases, such as liver cells and synoviocytes.

In general, the suitability of a candidate cleavable linking group can be evaluated by testing the ability of a degradative agent (or condition) to cleave the candidate linking group. It will also be desirable to also test the candidate cleavable linking group for the ability to resist cleavage in the blood or when in contact with other non-target tissue. Thus one can determine the relative susceptibility to cleavage between a first and a second condition, where the first is selected to be indicative of cleavage in a target cell and the second is selected to be indicative of cleavage in other tissues or biological fluids, e.g., blood or serum. The evaluations can be carried out in cell free systems, in cells, in cell culture, in organ or tissue culture, or in whole animals. It may be useful to make initial evaluations in cell-free or culture conditions and to confirm by further evaluations in whole animals. In preferred embodiments, useful candidate compounds are cleaved at least 2, 4, 10 or 100 times faster in the cell (or under in vitro conditions selected to mimic intracellular conditions) as compared to blood or serum (or under in vitro conditions selected to mimic extracellular conditions).

Redox Cleavable Linking Groups

One class of cleavable linking groups are redox cleavable linking groups that are cleaved upon reduction or oxidation. An example of reductively cleavable linking group is a disulphide linking group (—S—S—). To determine if a candidate cleavable linking group is a suitable "reductively cleavable linking group," or for example is suitable for use with a particular iRNA moiety and particular targeting agent one can look to methods described herein. For example, a candidate can be evaluated by incubation with dithiothreitol (DTT), or other reducing agent using reagents know in the art, which mimic the rate of cleavage which would be observed in a cell, e.g., a target cell. The candidates can also be evaluated under conditions which are selected to mimic blood or serum conditions. In a preferred embodiment, candidate compounds are cleaved by at most 10% in the blood. In preferred embodiments, useful candidate compounds are degraded at least 2, 4,

10 or 100 times faster in the cell (or under in vitro conditions selected to mimic intracellular conditions) as compared to blood (or under in vitro conditions selected to mimic extracellular conditions). The rate of cleavage of candidate compounds can be determined using standard enzyme kinetics assays under conditions chosen to mimic intracellular media and compared to conditions chosen to mimic extracellular media.

Phosphate-Based Cleavable Linking Groups

Phosphate-based cleavable linking groups are cleaved by agents that degrade or hydrolyze the phosphate group. An example of an agent that cleaves phosphate groups in cells are enzymes such as phosphatases in cells. Examples of phosphate-based linking groups are —O—P(O)(ORk)-O—, —O—P(S)(ORk)-O—, —O—P(S)(SRk)-O—, —S—P(O)(ORk)-O—, —O—P(O)(ORk)-S—, —S—P(O)(ORk)-S—, —O—P(S)(ORk)-S—, —S—P(S)(ORk)-O—, —O—P(O)(Rk)-O—, —O—P(S)(Rk)-O—, —S—P(O)(Rk)-O—, —S—P(S)(Rk)-O—, —S—P(O)(Rk)-S—, —O—P(S)(Rk)-S—. Preferred embodiments are —O—P(O)(OH)—O—, —O—P(S)(OH)—O—, —O—P(S)(SH)—O—, —S—P(O)(OH)—O—, —O—P(O)(OH)—S—, —S—P(O)(OH)—S—, —O—P(S)(OH)—S—, —S—P(S)(OH)—O—, —O—P(O)(H)—O—, —O—P(S)(H)—O—, —S—P(O)(H)—O—, —S—P(O)(H)—S—, —O—P(S)(H)—S—. A preferred embodiment is —O—P(O)(OH)—O—. These candidates can be evaluated using methods analogous to those described above.

Acid Cleavable Linking Groups

Acid cleavable linking groups are linking groups that are cleaved under acidic conditions. In preferred embodiments acid cleavable linking groups are cleaved in an acidic environment with a pH of about 6.5 or lower (e.g., about 6.0, 5.5, 5.0, or lower), or by agents such as enzymes that can act as a general acid. In a cell, specific low pH organelles, such as endosomes and lysosomes can provide a cleaving environment for acid cleavable linking groups. Examples of acid cleavable linking groups include but are not limited to hydrazones, esters, and esters of amino acids. Acid cleavable groups can have the general formula —C═NN—, C(O)O, or —OC(O). A preferred embodiment is when the carbon attached to the oxygen of the ester (the alkoxy group) is an aryl group, substituted alkyl group, or tertiary alkyl group such as dimethyl pentyl or t-butyl. These candidates can be evaluated using methods analogous to those described above.

Ester-Based Linking Groups

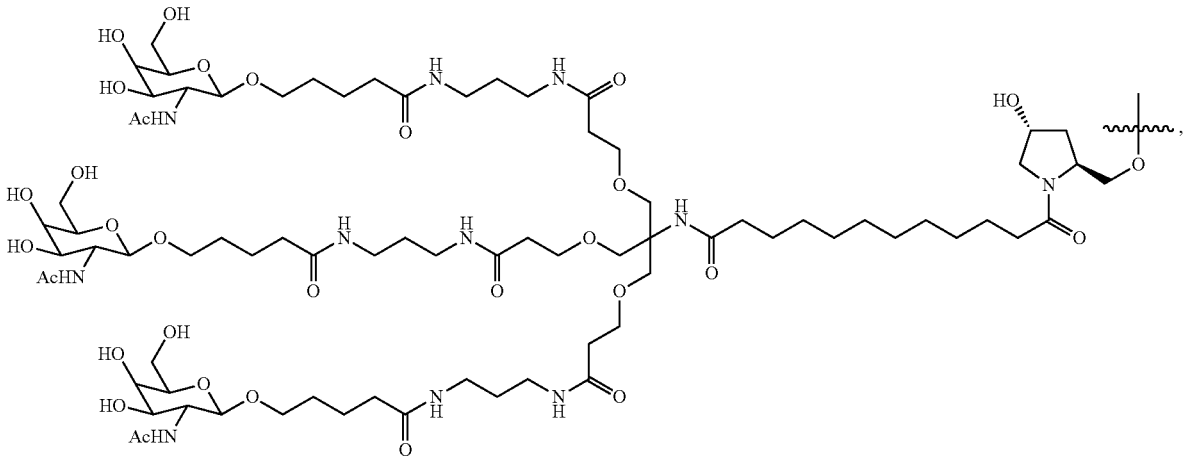
Ester-based cleavable linking groups are cleaved by enzymes such as esterases and amidases in cells. Examples of ester-based cleavable linking groups include but are not limited to esters of alkylene, alkenylene and alkynylene groups. Ester cleavable linking groups have the general formula —C(O)O—, or —OC(O)—. These candidates can be evaluated using methods analogous to those described above.

Peptide-Based Cleaving Groups

Peptide-based cleavable linking groups are cleaved by enzymes such as peptidases and proteases in cells. Peptide-based cleavable linking groups are peptide bonds formed between amino acids to yield oligopeptides (e.g., dipeptides, tripeptides etc.) and polypeptides. Peptide-based cleavable groups do not include the amide group (—C(O)NH—). The amide group can be formed between any alkylene, alkenylene or alkynelene. A peptide bond is a special type of amide bond formed between amino acids to yield peptides and proteins. The peptide based cleavage group is generally limited to the peptide bond (i.e., the amide bond) formed between amino acids yielding peptides and proteins and does not include the entire amide functional group. Peptide-based cleavable linking groups have the general formula —NHCHR^{A}C(O)NHCHR^{B}C(O)— (SEQ ID NO: 1107), where R^A and R^B are the R groups of the two adjacent amino acids. These candidates can be evaluated using methods analogous to those described above.

Representative carbohydrate conjugates with linkers include, but are not limited to,

(Formula XXIV)



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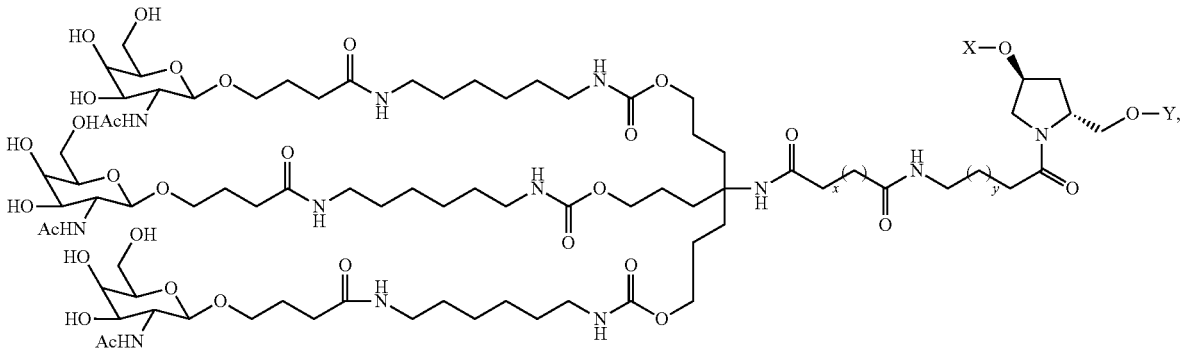
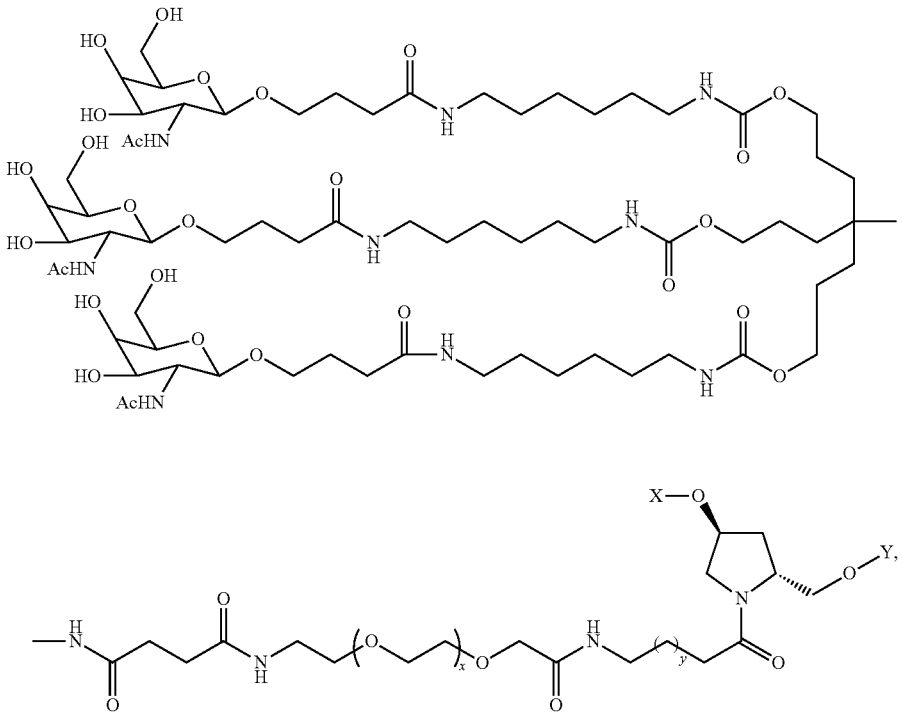
(Formula XXV)



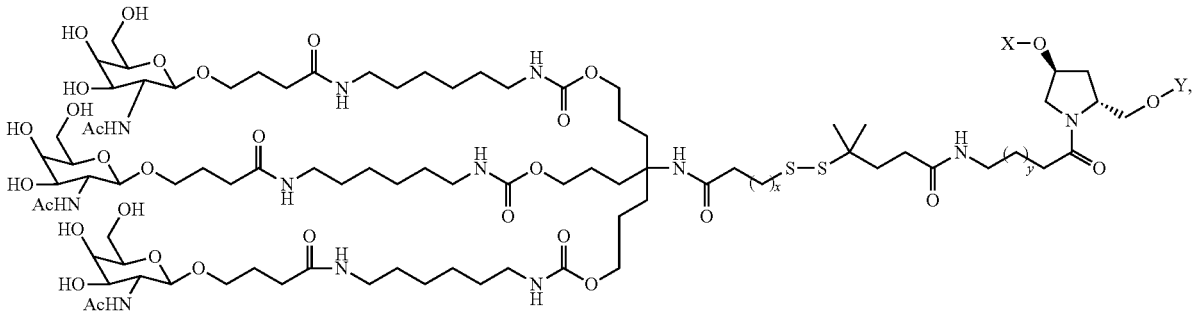
x = 1-30
y = 1-15

(Formula XXVI)



x = 1-30
y = 1-15

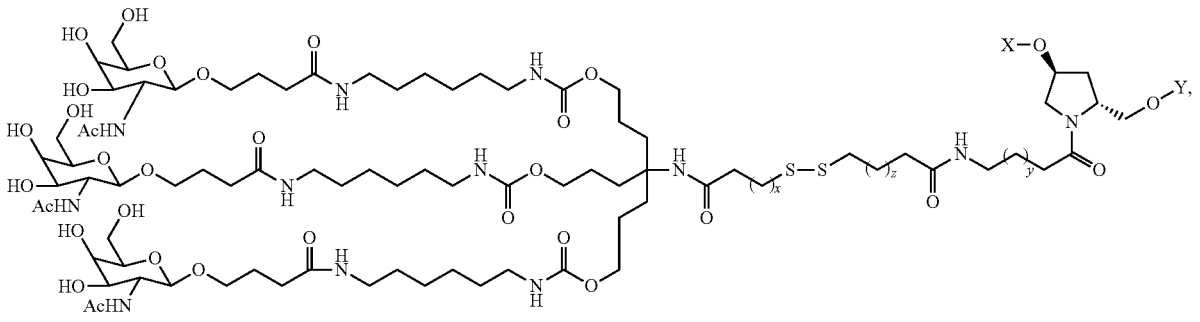
(Formula XXVII)



x = 0-30
y = 1-15

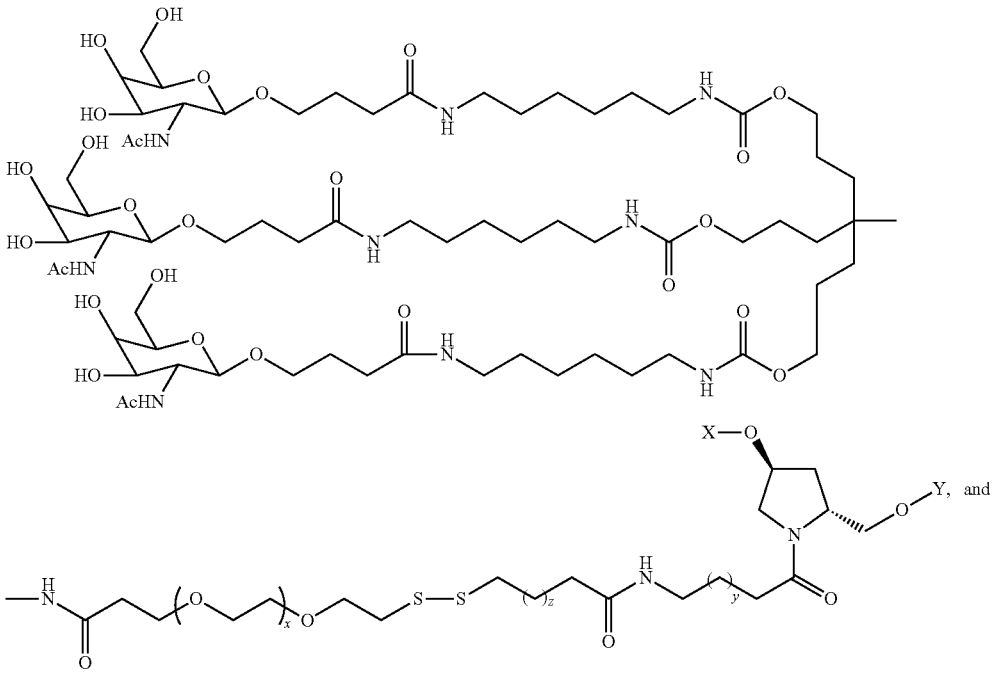
-continued

(Formula XXVIII)



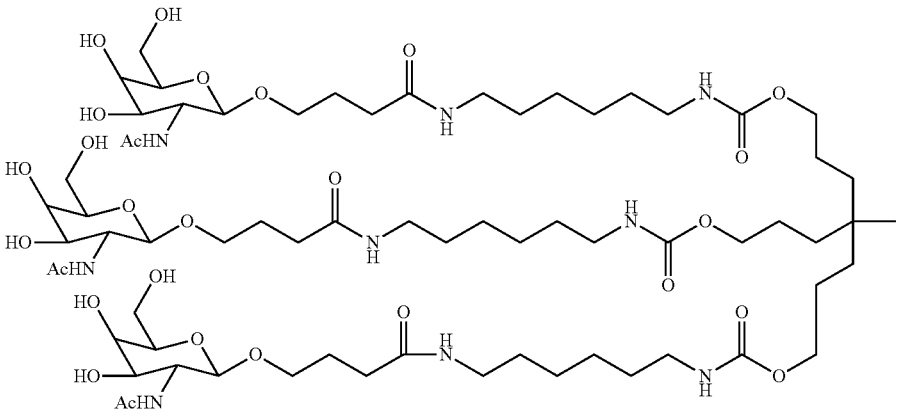
x = 0-30
y = 1-15
z = 1-20

(Formula XXIX)



x = 1-30
y = 1-15
z = 1-20

(Formula XXX)



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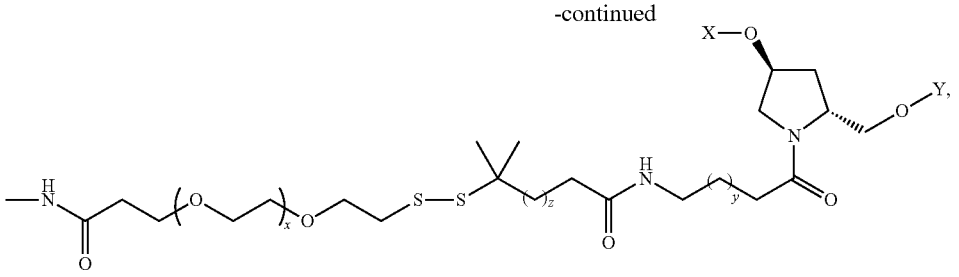


x = 1-30
y = 1-15
z = 1-20

when one of X or Y is an oligonucleotide, the other is a hydrogen.

Representative U.S. patents that teach the preparation of RNA conjugates include, but are not limited to, U.S. Pat. Nos. 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717, 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941; 6,294,664; 6,320,017; 6,576,752; 6,783,931; 6,900,297; 7,037,646; each of which is herein incorporated by reference.

It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications can be incorporated in a single compound or even at a single nucleoside within an iRNA. The present invention also includes iRNA compounds that are chimeric compounds. "Chimeric" iRNA compounds or "chimeras," in the context of this invention, are iRNA compounds, preferably dsRNAs, which contain two or more chemically distinct regions, each made up of at least one monomer unit, i.e., a nucleotide in the case of a dsRNA compound. These iRNAs typically contain at least one region wherein the RNA is modified so as to confer upon the iRNA increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target nucleic acid. An additional region of the iRNA may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of iRNA inhibition of gene expression. Consequently, comparable results can often be obtained with shorter iRNAs when chimeric dsRNAs are used, compared to phosphorothioate deoxy dsRNAs hybridizing to the same target region. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid hybridization techniques known in the art.

In certain instances, the RNA of an iRNA can be modified by a non-ligand group. A number of non-ligand molecules have been conjugated to iRNAs in order to enhance the activity, cellular distribution or cellular uptake of the iRNA, and procedures for performing such conjugations are available in the scientific literature. Such non-ligand moieties have included lipid moieties, such as cholesterol (Kubo, T. et al., Biochem. Biophys. Res. Comm., 2007, 365(1):54-61; Letsinger et al., Proc. Natl. Acad. Sci. USA, 1989, 86:6553), cholic acid (Manoharan et al., Bioorg. Med. Chem. Lett., 1994, 4:1053), a thioether, e.g., hexyl-S-tritylthiol (Manoharan et al., Ann. N.Y. Acad. Sci., 1992, 660:306; Manoharan et al., Bioorg. Med. Chem. Let., 1993, 3:2765), a thiocholesterol (Oberhauser et al., Nucl. Acids Res., 1992, 20:533), an aliphatic chain, e.g., dodecandiol or undecyl residues (Saison-Behmoaras et al., EMBO J., 1991, 10:111; Kabanov et al., FEBS Lett., 1990, 259:327; Svinarchuk et al., Biochimie, 1993, 75:49), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al., Tetrahedron Lett., 1995, 36:3651; Shea et al., Nucl. Acids Res., 1990, 18:3777), a polyamine or a polyethylene glycol chain (Manoharan et al., Nucleosides & Nucleotides, 1995, 14:969), or adamantane acetic acid (Manoharan et al., Tetrahedron Lett., 1995, 36:3651), a palmityl moiety (Mishra et al., Biochim. Biophys. Acta, 1995, 1264:229), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety (Crooke et al., J. Pharmacol. Exp. Ther., 1996, 277:923). Representative United States patents that teach the preparation of such RNA conjugates have been listed above. Typical conjugation protocols involve the synthesis of an RNAs bearing an aminolinker at one or more positions of the sequence. The amino group is then reacted with the molecule being conjugated using appropriate coupling or activating reagents. The conjugation reaction may be performed either with the RNA still bound to the solid support or following cleavage of the RNA, in solution phase. Purification of the RNA conjugate by HPLC typically affords the pure conjugate.

Delivery of iRNA

The delivery of an iRNA to a subject in need thereof can be achieved in a number of different ways. In vivo delivery can be performed directly by administering a composition comprising an iRNA, e.g. a dsRNA, to a subject. Alternatively, delivery can be performed indirectly by administering one or more vectors that encode and direct the expression of the iRNA.

Direct Delivery of an iRNA Composition

In general, any method of delivering a nucleic acid molecule can be adapted for use with an iRNA (see e.g., Akhtar S, and Julian R L. (1992) Trends Cell. Biol. 2(5):139-144 and WO94/02595, which are incorporated herein by reference in their entireties). However, there are three factors that are important to consider in order to successfully deliver an iRNA molecule in vivo: (a) biological stability of the delivered molecule, (2) preventing non-specific effects, and (3) accumulation of the delivered molecule in the target tissue. The non-specific effects of an iRNA can be minimized by local

administration, for example by direct injection or implantation into a tissue (as a non-limiting example, a tumor) or topically administering the preparation. Local administration to a treatment site maximizes local concentration of the agent, limits the exposure of the agent to systemic tissues that may otherwise be harmed by the agent or that may degrade the agent, and permits a lower total dose of the iRNA molecule to be administered. Several studies have shown successful knockdown of gene products when an iRNA is administered locally. For example, intraocular delivery of a VEGF dsRNA by intravitreal injection in cynomolgus monkeys (Tolentino, M J., et al (2004) Retina 24:132-138) and subretinal injections in mice (Reich, S J., et al (2003) Mol. Vis. 9:210-216) were both shown to prevent neovascularization in an experimental model of age-related macular degeneration. In addition, direct intratumoral injection of a dsRNA in mice reduces tumor volume (Pille, J., et al (2005) Mol. Ther. 11:267-274) and can prolong survival of tumor-bearing mice (Kim, W J., et al (2006) Mol. Ther. 14:343-350; Li, S., et al (2007) Mol. Ther. 15:515-523). RNA interference has also shown success with local delivery to the CNS by direct injection (Dorn, G., et al. (2004) Nucleic Acids 32:e49; Tan, P H., et al (2005) Gene Ther. 12:59-66; Makimura, H., et al (2002) BMC Neurosci. 3:18; Shishkina, G T., et al (2004) Neuroscience 129: 521-528; Thakker, E R., et al (2004) Proc. Natl. Acad. Sci. U.S.A. 101:17270-17275; Akaneya, Y., et al (2005) J. Neurophysiol. 93:594-602) and to the lungs by intranasal administration (Howard, K A., et al (2006) Mol. Ther. 14:476-484; Zhang, X., et al (2004) J. Biol. Chem. 279:10677-10684; Bitko, V., et al (2005) Nat. Med. 11:50-55). For administering an iRNA systemically for the treatment of a disease, the RNA can be modified or alternatively delivered using a drug delivery system; both methods act to prevent the rapid degradation of the dsRNA by endo- and exo-nucleases in vivo. Modification of the RNA or the pharmaceutical carrier can also permit targeting of the iRNA composition to the target tissue and avoid undesirable off-target effects. iRNA molecules can be modified by chemical conjugation to lipophilic groups such as cholesterol to enhance cellular uptake and prevent degradation. For example, an iRNA directed against ApoB conjugated to a lipophilic cholesterol moiety was injected systemically into mice and resulted in knockdown of apoB mRNA in both the liver and jejunum (Soutschek, J., et al (2004) Nature 432:173-178). Conjugation of an iRNA to an aptamer has been shown to inhibit tumor growth and mediate tumor regression in a mouse model of prostate cancer (McNamara, J O., et al (2006) Nat. Biotechnol. 24:1005-1015). In an alternative embodiment, the iRNA can be delivered using drug delivery systems such as a nanoparticle, a dendrimer, a polymer, liposomes, or a cationic delivery system. Positively charged cationic delivery systems facilitate binding of an iRNA molecule (negatively charged) and also enhance interactions at the negatively charged cell membrane to permit efficient uptake of an iRNA by the cell. Cationic lipids, dendrimers, or polymers can either be bound to an iRNA, or induced to form a vesicle or micelle (see e.g., Kim S H., et al (2008) Journal of Controlled Release 129(2):107-116) that encases an iRNA. The formation of vesicles or micelles further prevents degradation of the iRNA when administered systemically. Methods for making and administering cationic-iRNA complexes are well within the abilities of one skilled in the art (see e.g., Sorensen, D R., et al (2003) J. Mol. Biol 327:761-766; Verma, U N., et al (2003) Clin. Cancer Res. 9:1291-1300; Arnold, A S et al (2007) J. Hypertens. 25:197-205, which are incorporated herein by reference in their entirety). Some non-limiting examples of drug delivery systems useful for systemic delivery of iRNAs include DOTAP (Sorensen, DR., et al (2003), supra; Verma, U N., et al (2003), supra), Oligofectamine, "solid nucleic acid lipid particles" (Zimmermann, T S., et al (2006) Nature 441:111-114), cardiolipin (Chien, P Y., et al (2005) Cancer Gene Ther. 12:321-328; Pal, A., et al (2005) Int J. Oncol. 26:1087-1091), polyethyleneimine (Bonnet M E., et al (2008) Pharm. Res. August 16 Epub ahead of print; Aigner, A. (2006) J. Biomed. Biotechnol. 71659), Arg-Gly-Asp (RGD) peptides (Liu, S. (2006) Mol. Pharm. 3:472-487), and polyamidoamines (Tomalia, D A., et al (2007) Biochem. Soc. Trans. 35:61-67; Yoo, H., et al (1999) Pharm. Res. 16:1799-1804). In some embodiments, an iRNA forms a complex with cyclodextrin for systemic administration. Methods for administration and pharmaceutical compositions of iRNAs and cyclodextrins can be found in U.S. Pat. No. 7,427,605, which is herein incorporated by reference in its entirety.

Vector Encoded dsRNAs

In another aspect, iRNA targeting the Mylip/Idol gene can be expressed from transcription units inserted into DNA or RNA vectors (see, e.g., Couture, A, et al., *TIG.* (1996), 12:5-10; Skillern, A., et al., International PCT Publication No. WO 00/22113, Conrad, PCT Publication No. WO 00/22114, and Conrad, U.S. Pat. No. 6,054,299). Expression can be transient (on the order of hours to weeks) or sustained (weeks to months or longer), depending upon the specific construct used and the target tissue or cell type. These transgenes can be introduced as a linear construct, a circular plasmid, or a viral vector, which can be an integrating or non-integrating vector. The transgene can also be constructed to permit it to be inherited as an extrachromosomal plasmid (Gassmann, et al., *Proc. Natl. Acad. Sci. USA* (1995) 92:1292).

The individual strand or strands of an iRNA can be transcribed from a promoter on an expression vector. Where two separate strands are to be expressed to generate, for example, a dsRNA, two separate expression vectors can be co-introduced (e.g., by transfection or infection) into a target cell. Alternatively each individual strand of a dsRNA can be transcribed by promoters both of which are located on the same expression plasmid. In one embodiment, a dsRNA is expressed as inverted repeat polynucleotides joined by a linker polynucleotide sequence such that the dsRNA has a stem and loop structure.

iRNA expression vectors are generally DNA plasmids or viral vectors. Expression vectors compatible with eukaryotic cells, preferably those compatible with vertebrate cells, can be used to produce recombinant constructs for the expression of an iRNA as described herein. Eukaryotic cell expression vectors are well known in the art and are available from a number of commercial sources. Typically, such vectors are provided containing convenient restriction sites for insertion of the desired nucleic acid segment. Delivery of iRNA expressing vectors can be systemic, such as by intravenous or intramuscular administration, by administration to target cells ex-planted from the patient followed by reintroduction into the patient, or by any other means that allows for introduction into a desired target cell.

iRNA expression plasmids can be transfected into target cells as a complex with cationic lipid carriers (e.g., Oligofectamine) or non-cationic lipid-based carriers (e.g., Transit-TKO™). Multiple lipid transfections for iRNA-mediated knockdowns targeting different regions of a target RNA over a period of a week or more are also contemplated by the invention. Successful introduction of vectors into host cells can be monitored using various known methods. For example, transient transfection can be signaled with a reporter, such as a fluorescent marker, such as Green Fluorescent Protein (GFP). Stable transfection of cells ex vivo can

be ensured using markers that provide the transfected cell with resistance to specific environmental factors (e.g., antibiotics and drugs), such as hygromycin B resistance.

Viral vector systems which can be utilized with the methods and compositions described herein include, but are not limited to, (a) adenovirus vectors; (b) retrovirus vectors, including but not limited to lentiviral vectors, moloney murine leukemia virus, etc.; (c) adeno-associated virus vectors; (d) herpes simplex virus vectors; (e) SV 40 vectors; (f) polyoma virus vectors; (g) papilloma virus vectors; (h) picornavirus vectors; (i) pox virus vectors such as an *orthopox*, e.g., vaccinia virus vectors or avipox, e.g. canary pox or fowl pox; and (j) a helper-dependent or gutless adenovirus. Replication-defective viruses can also be advantageous. Different vectors will or will not become incorporated into the cells' genome. The constructs can include viral sequences for transfection, if desired. Alternatively, the construct may be incorporated into vectors capable of episomal replication, e.g. EPV and EBV vectors. Constructs for the recombinant expression of an iRNA will generally require regulatory elements, e.g., promoters, enhancers, etc., to ensure the expression of the iRNA in target cells. Other aspects to consider for vectors and constructs are further described below.

Vectors useful for the delivery of an iRNA will include regulatory elements (promoter, enhancer, etc.) sufficient for expression of the iRNA in the desired target cell or tissue. The regulatory elements can be chosen to provide either constitutive or regulated/inducible expression.

Expression of the iRNA can be precisely regulated, for example, by using an inducible regulatory sequence that is sensitive to certain physiological regulators, e.g., circulating glucose levels, or hormones (Docherty et al., 1994, FASEB J. 8:20-24). Such inducible expression systems, suitable for the control of dsRNA expression in cells or in mammals include, for example, regulation by ecdysone, by estrogen, progesterone, tetracycline, chemical inducers of dimerization, and isopropyl-beta-D1-thiogalactopyranoside (IPTG). A person skilled in the art would be able to choose the appropriate regulatory/promoter sequence based on the intended use of the iRNA transgene.

In a specific embodiment, viral vectors that contain nucleic acid sequences encoding an iRNA can be used. For example, a retroviral vector can be used (see Miller et al., Meth. Enzymol. 217:581-599 (1993)). These retroviral vectors contain the components necessary for the correct packaging of the viral genome and integration into the host cell DNA. The nucleic acid sequences encoding an iRNA are cloned into one or more vectors, which facilitates delivery of the nucleic acid into a patient. More detail about retroviral vectors can be found, for example, in Boesen et al., Biotherapy 6:291-302 (1994), which describes the use of a retroviral vector to deliver the mdr1 gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are: Clowes et al., J. Clin. Invest. 93:644-651 (1994); Kiem et al., Blood 83:1467-1473 (1994); Salmons and Gunzberg, Human Gene Therapy 4:129-141 (1993); and Grossman and Wilson, Curr. Opin. in Genetics and Devel. 3:110-114 (1993). Lentiviral vectors contemplated for use include, for example, the HIV based vectors described in U.S. Pat. Nos. 6,143,520; 5,665,557; and 5,981,276, which are herein incorporated by reference.

Adenoviruses are also contemplated for use in delivery of iRNAs. Adenoviruses are especially attractive vehicles, e.g., for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are liver, the central nervous system, endothelial cells, and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing cells. Kozarsky and Wilson, Current Opinion in Genetics and Development 3:499-503 (1993) present a review of adenovirus-based gene therapy. Bout et al., Human Gene Therapy 5:3-10 (1994) demonstrated the use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld et al., Science 252:431-434 (1991); Rosenfeld et al., Cell 68:143-155 (1992); Mastrangeli et al., J. Clin. Invest. 91:225-234 (1993); PCT Publication WO94/12649; and Wang, et al., Gene Therapy 2:775-783 (1995). A suitable AV vector for expressing an iRNA featured in the invention, a method for constructing the recombinant AV vector, and a method for delivering the vector into target cells, are described in Xia H et al. (2002), *Nat. Biotech.* 20: 1006-1010.

Use of Adeno-associated virus (AAV) vectors is also contemplated (Walsh et al., Proc. Soc. Exp. Biol. Med. 204:289-300 (1993); U.S. Pat. No. 5,436,146). In one embodiment, the iRNA can be expressed as two separate, complementary single-stranded RNA molecules from a recombinant AAV vector having, for example, either the U6 or H1 RNA promoters, or the cytomegalovirus (CMV) promoter. Suitable AAV vectors for expressing the dsRNA featured in the invention, methods for constructing the recombinant AV vector, and methods for delivering the vectors into target cells are described in Samulski R et al. (1987), J. Virol. 61: 3096-3101; Fisher K J et al. (1996), J. Virol, 70: 520-532; Samulski R et al. (1989), J. Virol. 63: 3822-3826; U.S. Pat. No. 5,252,479; U.S. Pat. No. 5,139,941; International Patent Application No. WO 94/13788; and International Patent Application No. WO 93/24641, the entire disclosures of which are herein incorporated by reference.

Another preferred viral vector is a pox virus such as a vaccinia virus, for example an attenuated vaccinia such as Modified Virus Ankara (MVA) or NYVAC, an avipox such as fowl pox or canary pox.

The tropism of viral vectors can be modified by pseudotyping the vectors with envelope proteins or other surface antigens from other viruses, or by substituting different viral capsid proteins, as appropriate. For example, lentiviral vectors can be pseudotyped with surface proteins from vesicular stomatitis virus (VSV), rabies, Ebola, Mokola, and the like. AAV vectors can be made to target different cells by engineering the vectors to express different capsid protein serotypes; see, e.g., Rabinowitz J E et al. (2002), J Virol 76:791-801, the entire disclosure of which is herein incorporated by reference.

The pharmaceutical preparation of a vector can include the vector in an acceptable diluent, or can include a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, e.g., retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

III. Pharmaceutical Compositions Containing Irna

In one embodiment, provided herein are pharmaceutical compositions containing an iRNA and a pharmaceutically acceptable carrier. The pharmaceutical composition containing the iRNA is useful for treating a disease or disorder associated with the expression or activity of a Mylip/Idol gene, such as pathological processes mediated by Mylip/Idol expression. Such pharmaceutical compositions are formulated based on the mode of delivery. One example is compositions that are formulated for systemic administration via parenteral delivery, e.g., by intravenous (IV) delivery.

Another example is compositions that are formulated for direct delivery into the brain parenchyma, e.g., by infusion into the brain, such as by continuous pump infusion.

The pharmaceutical compositions featured herein are administered in dosages sufficient to inhibit expression of Mylip/Idol genes. In general, a suitable dose of iRNA will be in the range of 0.01 to 200.0 milligrams per kilogram body weight of the recipient per day, generally in the range of 1 to 50 mg per kilogram body weight per day. For example, the dsRNA can be administered at 0.05 mg/kg, 0.5 mg/kg, 1 mg/kg, 1.5 mg/kg, 2 mg/kg, 3 mg/kg, 10 mg/kg, 20 mg/kg, 30 mg/kg, 40 mg/kg, or 50 mg/kg per single dose. The pharmaceutical composition may be administered once daily, or the iRNA may be administered as two, three, or more sub-doses at appropriate intervals throughout the day or even using continuous infusion or delivery through a controlled release formulation. In that case, the iRNA contained in each sub-dose must be correspondingly smaller in order to achieve the total daily dosage. The dosage unit can also be compounded for delivery over several days, e.g., using a conventional sustained release formulation which provides sustained release of the iRNA over a several day period. Sustained release formulations are well known in the art and are particularly useful for delivery of agents at a particular site, such as could be used with the agents of the present invention. In this embodiment, the dosage unit contains a corresponding multiple of the daily dose.

The effect of a single dose on Mylip/Idol levels can be long lasting, such that subsequent doses are administered at not more than 3, 4, or 5 day intervals, or at not more than 1, 2, 3, or 4 week intervals.

The skilled artisan will appreciate that certain factors may influence the dosage and timing required to effectively treat a subject, including but not limited to the severity of the disease or disorder, previous treatments, the general health and/or age of the subject, and other diseases present. Moreover, treatment of a subject with a therapeutically effective amount of a composition can include a single treatment or a series of treatments. Estimates of effective dosages and in vivo half-lives for the individual iRNAs encompassed by the invention can be made using conventional methodologies or on the basis of in vivo testing using an appropriate animal model, as described elsewhere herein.

Advances in mouse genetics have generated a number of mouse models for the study of various human diseases, such as pathological processes mediated by Mylip/Idol expression. Such models can be used for in vivo testing of iRNA, as well as for determining a therapeutically effective dose. A suitable mouse model is, for example, a mouse containing a transgene expressing human Mylip/Idol.

The present invention also includes pharmaceutical compositions and formulations that include the iRNA compounds featured in the invention. The pharmaceutical compositions of the present invention may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be topical (e.g., by a transdermal patch), pulmonary, e.g., by inhalation or insufflation of powders or aerosols, including by nebulizer; intratracheal, intranasal, epidermal and transdermal, oral or parenteral. Parenteral administration includes intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion; subdermal, e.g., via an implanted device; or intracranial, e.g., by intraparenchymal, intrathecal or intraventricular, administration.

The iRNA can be delivered in a manner to target a particular tissue, such as the liver (e.g., the hepatocytes of the liver).

Pharmaceutical compositions and formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable. Coated condoms, gloves and the like may also be useful. Suitable topical formulations include those in which the iRNAs featured in the invention are in admixture with a topical delivery agent such as lipids, liposomes, fatty acids, fatty acid esters, steroids, chelating agents and surfactants. Suitable lipids and liposomes include neutral (e.g., dioleoylphosphatidyl DOPE ethanolamine, dimyristoylphosphatidyl choline DMPC, distearolyphosphatidyl choline) negative (e.g., dimyristoylphosphatidyl glycerol DMPG) and cationic (e.g., dioleoyltetramethylaminopropyl DOTAP and dioleoylphosphatidyl ethanolamine DOTMA). iRNAs featured in the invention may be encapsulated within liposomes or may form complexes thereto, in particular to cationic liposomes. Alternatively, iRNAs may be complexed to lipids, in particular to cationic lipids. Suitable fatty acids and esters include but are not limited to arachidonic acid, oleic acid, eicosanoic acid, lauric acid, caprylic acid, capric acid, myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein, dilaurin, glyceryl 1-monocaprate, 1-dodecylazacycloheptan-2-one, an acylcarnitine, an acylcholine, or a C_{1-20} alkyl ester (e.g., isopropylmyristate IPM), monoglyceride, diglyceride or pharmaceutically acceptable salt thereof. Topical formulations are described in detail in U.S. Pat. No. 6,747,014, which is incorporated herein by reference.

Liposomal Formulations

There are many organized surfactant structures besides microemulsions that have been studied and used for the formulation of drugs. These include monolayers, micelles, bilayers and vesicles. Vesicles, such as liposomes, have attracted great interest because of their specificity and the duration of action they offer from the standpoint of drug delivery. As used in the present invention, the term "liposome" means a vesicle composed of amphiphilic lipids arranged in a spherical bilayer or bilayers.

Liposomes are unilamellar or multilamellar vesicles which have a membrane formed from a lipophilic material and an aqueous interior. The aqueous portion contains the composition to be delivered. Cationic liposomes possess the advantage of being able to fuse to the cell wall. Non-cationic liposomes, although not able to fuse as efficiently with the cell wall, are taken up by macrophages in vivo.

In order to traverse intact mammalian skin, lipid vesicles must pass through a series of fine pores, each with a diameter less than 50 nm, under the influence of a suitable transdermal gradient. Therefore, it is desirable to use a liposome which is highly deformable and able to pass through such fine pores.

Further advantages of liposomes include; liposomes obtained from natural phospholipids are biocompatible and biodegradable; liposomes can incorporate a wide range of water and lipid soluble drugs; liposomes can protect encapsulated drugs in their internal compartments from metabolism and degradation (Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245). Important considerations in the preparation of liposome formulations are the lipid surface charge, vesicle size and the aqueous volume of the liposomes.

Liposomes are useful for the transfer and delivery of active ingredients to the site of action. Because the liposomal membrane is structurally similar to biological membranes, when liposomes are applied to a tissue, the liposomes start to merge

with the cellular membranes and as the merging of the liposome and cell progresses, the liposomal contents are emptied into the cell where the active agent may act.

Liposomal formulations have been the focus of extensive investigation as the mode of delivery for many drugs. There is growing evidence that for topical administration, liposomes present several advantages over other formulations. Such advantages include reduced side-effects related to high systemic absorption of the administered drug, increased accumulation of the administered drug at the desired target, and the ability to administer a wide variety of drugs, both hydrophilic and hydrophobic, into the skin.

Several reports have detailed the ability of liposomes to deliver agents including high-molecular weight DNA into the skin. Compounds including analgesics, antibodies, hormones and high-molecular weight DNAs have been administered to the skin. The majority of applications resulted in the targeting of the upper epidermis

Liposomes fall into two broad classes. Cationic liposomes are positively charged liposomes which interact with the negatively charged DNA molecules to form a stable complex. The positively charged DNA/liposome complex binds to the negatively charged cell surface and is internalized in an endosome. Due to the acidic pH within the endosome, the liposomes are ruptured, releasing their contents into the cell cytoplasm (Wang et al., Biochem. Biophys. Res. Commun., 1987, 147, 980-985).

Liposomes which are pH-sensitive or negatively-charged, entrap nucleic acids rather than complex with it. Since both the DNA and the lipid are similarly charged, repulsion rather than complex formation occurs. Nevertheless, some DNA is entrapped within the aqueous interior of these liposomes. pH-sensitive liposomes have been used to deliver nucleic acids encoding the thymidine kinase gene to cell monolayers in culture. Expression of the exogenous gene was detected in the target cells (Zhou et al., Journal of Controlled Release, 1992, 19, 269-274).

One major type of liposomal composition includes phospholipids other than naturally-derived phosphatidylcholine. Neutral liposome compositions, for example, can be formed from dimyristoyl phosphatidylcholine (DMPC) or dipalmitoyl phosphatidylcholine (DPPC). Anionic liposome compositions generally are formed from dimyristoyl phosphatidylglycerol, while anionic fusogenic liposomes are formed primarily from dioleoyl phosphatidylethanolamine (DOPE). Another type of liposomal composition is formed from phosphatidylcholine (PC) such as, for example, soybean PC, and egg PC. Another type is formed from mixtures of phospholipid and/or phosphatidylcholine and/or cholesterol.

Several studies have assessed the topical delivery of liposomal drug formulations to the skin. Application of liposomes containing interferon to guinea pig skin resulted in a reduction of skin herpes sores while delivery of interferon via other means (e.g., as a solution or as an emulsion) were ineffective (Weiner et al., Journal of Drug Targeting, 1992, 2, 405-410). Further, an additional study tested the efficacy of interferon administered as part of a liposomal formulation to the administration of interferon using an aqueous system, and concluded that the liposomal formulation was superior to aqueous administration (du Plessis et al., Antiviral Research, 1992, 18, 259-265).

Non-ionic liposomal systems have also been examined to determine their utility in the delivery of drugs to the skin, in particular systems comprising non-ionic surfactant and cholesterol. Non-ionic liposomal formulations comprising Novasome™ I (glyceryl dilaurate/cholesterol/polyoxyethylene-10-stearyl ether) and Novasome™ II (glyceryl distearate/cholesterol/polyoxyethylene-10-stearyl ether) were used to deliver cyclosporin-A into the dermis of mouse skin. Results indicated that such non-ionic liposomal systems were effective in facilitating the deposition of cyclosporine A into different layers of the skin (Hu et al. S. T. P. Pharma. Sci., 1994, 4, 6, 466).

Liposomes also include "sterically stabilized" liposomes, a term which, as used herein, refers to liposomes comprising one or more specialized lipids that, when incorporated into liposomes, result in enhanced circulation lifetimes relative to liposomes lacking such specialized lipids. Examples of sterically stabilized liposomes are those in which part of the vesicle-forming lipid portion of the liposome (A) comprises one or more glycolipids, such as monosialoganglioside G_{M1}, or (B) is derivatized with one or more hydrophilic polymers, such as a polyethylene glycol (PEG) moiety. While not wishing to be bound by any particular theory, it is thought in the art that, at least for sterically stabilized liposomes containing gangliosides, sphingomyelin, or PEG-derivatized lipids, the enhanced circulation half-life of these sterically stabilized liposomes derives from a reduced uptake into cells of the reticuloendothelial system (RES) (Allen et al., FEBS Letters, 1987, 223, 42; Wu et al., Cancer Research, 1993, 53, 3765).

Various liposomes comprising one or more glycolipids are known in the art. Papahadjopoulos et al. (Ann. N.Y. Acad. Sci., 1987, 507, 64) reported the ability of monosialoganglioside G_{M1}, galactocerebroside sulfate and phosphatidylinositol to improve blood half-lives of liposomes. These findings were expounded upon by Gabizon et al. (Proc. Natl. Acad. Sci. U.S.A., 1988, 85, 6949). U.S. Pat. No. 4,837,028 and WO 88/04924, both to Allen et al., disclose liposomes comprising (1) sphingomyelin and (2) the ganglioside G_{M1} or a galactocerebroside sulfate ester. U.S. Pat. No. 5,543,152 (Webb et al.) discloses liposomes comprising sphingomyelin. Liposomes comprising 1,2-sn-dimyristoylphosphatidylcholine are disclosed in WO 97/13499 (Lim et al).

Many liposomes comprising lipids derivatized with one or more hydrophilic polymers, and methods of preparation thereof, are known in the art. Sunamoto et al. (Bull. Chem. Soc. Jpn., 1980, 53, 2778) described liposomes comprising a nonionic detergent, $2C_{1215G}$, that contains a PEG moiety. Illum et al. (FEBS Lett., 1984, 167, 79) noted that hydrophilic coating of polystyrene particles with polymeric glycols results in significantly enhanced blood half-lives. Synthetic phospholipids modified by the attachment of carboxylic groups of polyalkylene glycols (e.g., PEG) are described by Sears (U.S. Pat. Nos. 4,426,330 and 4,534,899). Klibanov et al. (FEBS Lett., 1990, 268, 235) described experiments demonstrating that liposomes comprising phosphatidylethanolamine (PE) derivatized with PEG or PEG stearate have significant increases in blood circulation half-lives. Blume et al. (Biochimica et Biophysica Acta, 1990, 1029, 91) extended such observations to other PEG-derivatized phospholipids, e.g., DSPE-PEG, formed from the combination of distearoylphosphatidylethanolamine (DSPE) and PEG. Liposomes having covalently bound PEG moieties on their external surface are described in European Patent No. EP 0 445 131 B1 and WO 90/04384 to Fisher. Liposome compositions containing 1-20 mole percent of PE derivatized with PEG, and methods of use thereof, are described by Woodle et al. (U.S. Pat. Nos. 5,013,556 and 5,356,633) and Martin et al. (U.S. Pat. No. 5,213,804 and European Patent No. EP 0 496 813 B1). Liposomes comprising a number of other lipid-polymer conjugates are disclosed in WO 91/05545 and U.S. Pat. No. 5,225,212 (both to Martin et al.) and in WO 94/20073 (Zalipsky et al.) Liposomes comprising PEG-modified ceramide lipids are described in WO 96/10391 (Choi et al). U.S.

Pat. No. 5,540,935 (Miyazaki et al.) and U.S. Pat. No. 5,556,948 (Tagawa et al.) describes PEG-containing liposomes that can be further derivatized with functional moieties on their surfaces.

A number of liposomes comprising nucleic acids are known in the art. WO 96/40062 to Thierry et al. discloses methods for encapsulating high molecular weight nucleic acids in liposomes. U.S. Pat. No. 5,264,221 to Tagawa et al. discloses protein-bonded liposomes and asserts that the contents of such liposomes may include a dsRNA. U.S. Pat. No. 5,665,710 to Rahman et al. describes certain methods of encapsulating oligodeoxynucleotides in liposomes. WO 97/04787 to Love et al. discloses liposomes comprising dsRNAs targeted to the raf gene.

Transfersomes are yet another type of liposomes, and are highly deformable lipid aggregates which are attractive candidates for drug delivery vehicles. Transfersomes may be described as lipid droplets which are so highly deformable that they are easily able to penetrate through pores which are smaller than the droplet. Transfersomes are adaptable to the environment in which they are used, e.g., they are self-optimizing (adaptive to the shape of pores in the skin), self-repairing, frequently reach their targets without fragmenting, and often self-loading. To make transfersomes it is possible to add surface edge-activators, usually surfactants, to a standard liposomal composition. Transfersomes have been used to deliver serum albumin to the skin. The transfersome-mediated delivery of serum albumin has been shown to be as effective as subcutaneous injection of a solution containing serum albumin.

Surfactants find wide application in formulations such as emulsions (including microemulsions) and liposomes. The most common way of classifying and ranking the properties of the many different types of surfactants, both natural and synthetic, is by the use of the hydrophile/lipophile balance (HLB). The nature of the hydrophilic group (also known as the "head") provides the most useful means for categorizing the different surfactants used in formulations (Rieger, in Pharmaceutical Dosage Forms, Marcel Dekker, Inc., New York, N.Y., 1988, p. 285).

If the surfactant molecule is not ionized, it is classified as a nonionic surfactant. Nonionic surfactants find wide application in pharmaceutical and cosmetic products and are usable over a wide range of pH values. In general their HLB values range from 2 to about 18 depending on their structure. Nonionic surfactants include nonionic esters such as ethylene glycol esters, propylene glycol esters, glyceryl esters, polyglyceryl esters, sorbitan esters, sucrose esters, and ethoxylated esters. Nonionic alkanolamides and ethers such as fatty alcohol ethoxylates, propoxylated alcohols, and ethoxylated/propoxylated block polymers are also included in this class. The polyoxyethylene surfactants are the most popular members of the nonionic surfactant class.

If the surfactant molecule carries a negative charge when it is dissolved or dispersed in water, the surfactant is classified as anionic. Anionic surfactants include carboxylates such as soaps, acyl lactylates, acyl amides of amino acids, esters of sulfuric acid such as alkyl sulfates and ethoxylated alkyl sulfates, sulfonates such as alkyl benzene sulfonates, acyl isethionates, acyl taurates and sulfosuccinates, and phosphates. The most important members of the anionic surfactant class are the alkyl sulfates and the soaps.

If the surfactant molecule carries a positive charge when it is dissolved or dispersed in water, the surfactant is classified as cationic. Cationic surfactants include quaternary ammonium salts and ethoxylated amines. The quaternary ammonium salts are the most used members of this class.

If the surfactant molecule has the ability to carry either a positive or negative charge, the surfactant is classified as amphoteric. Amphoteric surfactants include acrylic acid derivatives, substituted alkylamides, N-alkylbetaines and phosphatides.

The use of surfactants in drug products, formulations and in emulsions has been reviewed (Rieger, in Pharmaceutical Dosage Forms, Marcel Dekker, Inc., New York, N.Y., 1988, p. 285).

Nucleic Acid Lipid Particles

In one embodiment, an Idol/Mylip dsRNA featured in the invention is fully encapsulated in the lipid formulation, e.g., to form a SPLP, pSPLP, SNALP, or other nucleic acid-lipid particle. As used herein, the term "SNALP" refers to a stable nucleic acid-lipid particle, including SPLP. As used herein, the term "SPLP" refers to a nucleic acid-lipid particle comprising plasmid DNA encapsulated within a lipid vesicle. SNALPs and SPLPs typically contain a cationic lipid, a non-cationic lipid, and a lipid that prevents aggregation of the particle (e.g., a PEG-lipid conjugate). SNALPs and SPLPs are extremely useful for systemic applications, as they exhibit extended circulation lifetimes following intravenous (i.v.) injection and accumulate at distal sites (e.g., sites physically separated from the administration site). SPLPs include "pSPLP," which include an encapsulated condensing agent-nucleic acid complex as set forth in PCT Publication No. WO 00/03683. The particles of the present invention typically have a mean diameter of about 50 nm to about 150 nm, more typically about 60 nm to about 130 nm, more typically about 70 nm to about 110 nm, most typically about 70 nm to about 90 nm, and are substantially nontoxic. In addition, the nucleic acids when present in the nucleic acid-lipid particles of the present invention are resistant in aqueous solution to degradation with a nuclease. Nucleic acid-lipid particles and their method of preparation are disclosed in, e.g., U.S. Pat. Nos. 5,976,567; 5,981,501; 6,534,484; 6,586,410; 6,815,432; and PCT Publication No. WO 96/40964.

In one embodiment, the lipid to drug ratio (mass/mass ratio) (e.g., lipid to dsRNA ratio) will be in the range of from about 1:1 to about 50:1, from about 1:1 to about 25:1, from about 3:1 to about 15:1, from about 4:1 to about 10:1, from about 5:1 to about 9:1, or about 6:1 to about 9:1.

The cationic lipid can be, for example, N,N-dioleyl-N,N-dimethylammonium chloride (DODAC), N,N-distearyl-N,N-dimethylammonium bromide (DDAB), N-(I-(2,3-dioleoyloxy)propyl)-N,N,N-trimethylammonium chloride (DOTAP), N-(I-(2,3-dioleyloxy)propyl)-N,N,N-trimethylammonium chloride (DOTMA), N,N-dimethyl-2,3-dioleyloxy)propylamine (DODMA), 1,2-DiLinoleyloxy-N,N-dimethylaminopropane (DLinDMA), 1,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLenDMA), 1,2-Dilinoleylcarbamoyloxy-3-dimethylaminopropane (DLin-C-DAP), 1,2-Dilinoleyoxy-3-(dimethylamino) acetoxypropane (DLin-DAC), 1,2-Dilinoleyoxy-3-morpholinopropane (DLin-MA), 1,2-Dilinoleoyl-3-

dimethylaminopropane (DLinDAP), 1,2-Dilinoleylthio-3-dimethylaminopropane (DLin-S-DMA), 1-Linoleoyl-2-linoleyloxy-3-dimethylaminopropane (DLin-2-DMAP), 1,2-Dilinoleyloxy-3-trimethylaminopropane chloride salt (DLin-TMA.Cl), 1,2-Dilinoleoyl-3-trimethylaminopropane chloride salt (DLin-TAP.Cl), 1,2-Dilinoleyloxy-3-(N-methylpiperazino)propane (DLin-MPZ), or 3-(N,N-Dilinoleylamino)-1,2-propanediol (DLinAP), 3-(N,N-Dioleylamino)-1,2-propanedio (DOAP), 1,2-Dilinoleyloxo-3-(2-N,N-dimethylamino)ethoxypropane (DLin-EG-DMA), 1,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLinDMA), 2,2-Dilinoleyl-4-dimethylaminomethyl-[1,3]-dioxolane (DLin-K-DMA) or analogs thereof, (3aR,5s,6aS)-N,N-dimethyl-2,2-di((9Z,12Z)-octadeca-9,12-dienyl)tetrahydro-3aH-cyclopenta[d][1,3]dioxol-5-amine (ALN100), (6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-yl 4-(dimethylamino)butanoate (MC3), 1,1'-(2-(4-(2-((2-(bis(2-hydroxydodecyl)amino)ethyl)(2-hydroxydodecyl)amino)ethyl)piperazin-1-yl)ethylazanediyl)didodecan-2-ol (Tech G1), or a mixture thereof. The cationic lipid may comprise from about 20 mol % to about 50 mol % or about 40 mol % of the total lipid present in the particle.

In another embodiment, the compound 2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane can be used to prepare lipid-siRNA nanoparticles. Synthesis of 2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane is described in U.S. provisional patent application No. 61/107,998 filed on Oct. 23, 2008, which is herein incorporated by reference.

In one embodiment, the lipid-siRNA particle includes 40% 2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane: 10% DSPC: 40% Cholesterol: 10% PEG-C-DOMG (mole percent) with a particle size of 63.0±20 nm and a 0.027 siRNA/Lipid Ratio.

The non-cationic lipid may be an anionic lipid or a neutral lipid including, but not limited to, distearoylphosphatidylcholine (DSPC), dioleoylphosphatidylcholine (DOPC), dipalmitoylphosphatidylcholine (DPPC), dioleoylphosphatidylglycerol (DOPG), dipalmitoylphosphatidylglycerol (DPPG), dioleoyl-phosphatidylethanolamine (DOPE), palmitoyloleoylphosphatidylcholine (POPC), palmitoyloleoylphosphatidylethanolamine (POPE), dioleoyl-phosphatidylethanolamine 4-(N-maleimidomethyl)-cyclohexane-1-carboxylate (DOPE-mal), dipalmitoyl phosphatidyl ethanolamine (DPPE), dimyristoylphosphoethanolamine (DMPE), distearoyl-phosphatidyl-ethanolamine (DSPE), 16-O-monomethyl PE, 16-O-dimethyl PE, 18-1-trans PE, 1-stearoyl-2-oleoyl-phosphatidyethanolamine (SOPE), cholesterol, or a mixture thereof. The non-cationic lipid may be from about 5 mol % to about 90 mol %, about 10 mol %, or about 58 mol % if cholesterol is included, of the total lipid present in the particle.

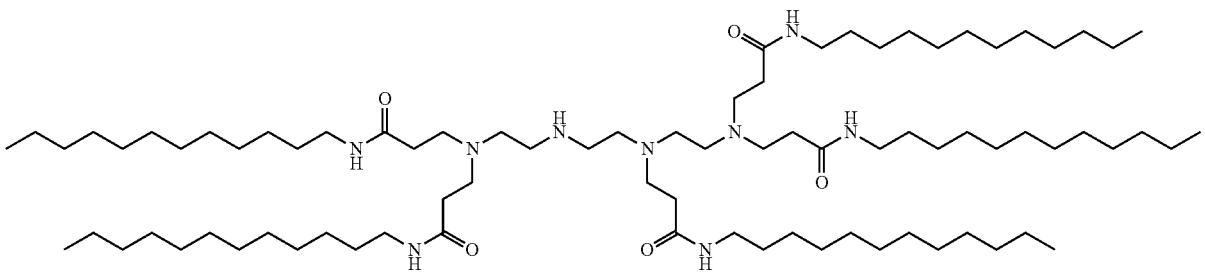
The conjugated lipid that inhibits aggregation of particles may be, for example, a polyethyleneglycol (PEG)-lipid including, without limitation, a PEG-diacylglycerol (DAG), a PEG-dialkyloxypropyl (DAA), a PEG-phospholipid, a PEG-ceramide (Cer), or a mixture thereof. The PEG-DAA conjugate may be, for example, a PEG-dilauryloxypropyl (C_{12}), a PEG-dimyristyloxypropyl (C_{14}), a PEG-dipalmityloxypropyl (C_{16}), or a PEG-distearyloxypropyl (C_{18}). The conjugated lipid that prevents aggregation of particles may be from 0 mol % to about 20 mol % or about 2 mol % of the total lipid present in the particle.

In some embodiments, the nucleic acid-lipid particle further includes cholesterol at, e.g., about 10 mol % to about 60 mol % or about 48 mol % of the total lipid present in the particle.

LNP01

In one embodiment, the lipidoid ND98.4HCl (MW 1487) (see U.S. patent application Ser. No. 12/056,230, filed Mar. 26, 2008, which is herein incorporated by reference in its entirety), Cholesterol (Sigma-Aldrich), and PEG-Ceramide C16 (Avanti Polar Lipids) can be used to prepare lipid-dsRNA nanoparticles (i.e., LNP01 particles). Stock solutions of each in ethanol can be prepared as follows: ND98, 133 mg/ml; Cholesterol, 25 mg/ml, PEG-Ceramide C16, 100 mg/ml. The ND98, Cholesterol, and PEG-Ceramide C16 stock solutions can then be combined in a, e.g., 42:48:10 molar ratio. The combined lipid solution can be mixed with aqueous dsRNA (e.g., in sodium acetate pH 5) such that the final ethanol concentration is about 35-45% and the final sodium acetate concentration is about 100-300 mM. Lipid-dsRNA nanoparticles typically form spontaneously upon mixing. Depending on the desired particle size distribution, the resultant nanoparticle mixture can be extruded through a polycarbonate membrane (e.g., 100 nm cut-off) using, for example, a thermobarrel extruder, such as Lipex Extruder (Northern Lipids, Inc). In some cases, the extrusion step can be omitted. Ethanol removal and simultaneous buffer exchange can be accomplished by, for example, dialysis or tangential flow filtration. Buffer can be exchanged with, for example, phosphate buffered saline (PBS) at about pH 7, e.g., about pH 6.9, about pH 7.0, about pH 7.1, about pH 7.2, about pH 7.3, or about pH 7.4.

Formula I



ND98 Isomer I

LNP01 formulations are described, e.g., in International Application Publication No. WO 2008/042973, which is hereby incorporated by reference.

Additional exemplary lipid-dsRNA formulations are as follows:

	Cationic Lipid	cationic lipid/non-cationic lipid/cholesterol/PEG-lipid conjugate Lipid:siRNA ratio
SNALP-1	1,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLinDMA)	DLinDMA/DPPC/Cholesterol/PEG-cDMA (57.1/7.1/34.4/1.4) lipid:siRNA ~7:1
S-XTC	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)	XTC/DPPC/CholesteroyPEG-cDMA 57.1/7.1/34.4/1.4 lipid:siRNA ~7:1
LNP05	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)	XTC/DSPC/Cholesterol/PEG-DMG 57.5/7.5/31.5/3.5 lipid:siRNA ~6:1
LNP06	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)	XTC/DSPC/Cholesterol/PEG-DMG 57.5/7.5/31.5/3.5 lipid:siRNA ~11:1
LNP07	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)	XTC/DSPC/Cholesterol/PEG-DMG 60/7.5/31/1.5, lipid:siRNA ~6:1
LNP08	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)	XTC/DSPC/Cholesterol/PEG-DMG 60/7.5/31/1.5, lipid:siRNA ~11:1
LNP09	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)	XTC/DSPC/Cholesterol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA 10:1
LNP10	(3aR,5s,6aS)-N,N-dimethyl-2,2-di((9Z,12Z)-octadeca-9,12-dienyl)tetrahydro-3aH-cyclopenta[d][1,3]dioxol-5-amine (ALN100)	ALN100/DSPC/Cholesterol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA 10:1
LNP11	(6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-yl 4-(dimethylamino)butanoate (MC3)	MC-3/DSPC/Cholesterol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA 10:1
LNP12	1,1'-(2-(4-(2-((2-(bis(2-hydroxydodecyl)amino)ethyl)(2-hydroxydodecyl)amino)ethyl)piperazin-1-yl)ethylazanediyl)didodecan-2-ol (C12-200)	C12-200/DSPC/Cholesterol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA 10:1
LNP13	XTC	XTC/DSPC/Chol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA: 33:1
LNP14	MC3	MC3/DSPC/Chol/PEG-DMG 40/15/40/5 Lipid:siRNA: 11:1
LNP15	MC3	MC3/DSPC/Chol/PEG-DSG/GalNAc-PEG-DSG 50/10/35/4.5/0.5 Lipid:siRNA: 11:1
LNP16	MC3	MC3/DSPC/Chol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA: 7:1
LNP17	MC3	MC3/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 10:1
LNP18	MC3	MC3/DSPC/Chol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA: 12:1
LNP19	MC3	MC3/DSPC/Chol/PEG-DMG 50/10/35/5 Lipid:siRNA: 8:1
LNP20	MC3	MC3/DSPC/Chol/PEG-DPG 50/10/38.5/1.5 Lipid:siRNA: 10:1
LNP21	C12-200	C12-200/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 7:1

-continued

	Cationic Lipid	cationic lipid/non-cationic lipid/cholesterol/PEG-lipid conjugate Lipid:siRNA ratio
LNP22	XTC	XTC/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 10:1

DSPC: distearoylphosphatidylcholine

DPPC: dipalmitoylphosphatidylcholine

PEG-DMG: PEG-didimyristoyl glycerol (C14-PEG, or PEG-C14) (PEG with avg mol wt of 2000)

PEG-DSG: PEG-distyryl glycerol (C18-PEG, or PEG-C18) (PEG with avg mol wt of 2000)

PEG-cDMA: PEG-carbamoyl-1,2-dimyristyloxypropylamine (PEG with avg mol wt of 2000)

SNALP (1,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLinDMA)) comprising formulations are described in International Publication No. WO2009/127060, filed Apr. 15, 2009, which is hereby incorporated by reference.

XTC comprising formulations are described, e.g., in U.S. Provisional Ser. No. 61/239,686, filed Sep. 3, 2009, which is hereby incorporated by reference.

MC3 comprising formulations are described, e.g., in U.S. Provisional Ser. No. 61/244,834, filed Sep. 22, 2009, U.S. Provisional Ser. No. 61/185,800, filed Jun. 10, 2009, and International Application No. PCT/US10/28224, filed Jun. 10, 2010, which are hereby incorporated by reference.

ALNY-100 comprising formulations are described, e.g., International patent application number PCT/US09/63933, filed on Nov. 10, 2009, which is hereby incorporated by reference.

C12-200 comprising formulations are described in U.S. Provisional Ser. No. 61/175,770, filed May 5, 2009and International Application No. PCT/US10/33777, filed May 5, 2010, which are hereby incorporated by reference.

Synthesis of Cationic Lipids

Any of the compounds, e.g., cationic lipids and the like, used in the nucleic acid-lipid particles of the invention can be prepared by known organic synthesis techniques, including the methods described in more detail in the Examples. All substituents are as defined below unless indicated otherwise.

"Alkyl" means a straight chain or branched, noncyclic or cyclic, saturated aliphatic hydrocarbon containing from 1 to 24 carbon atoms. Representative saturated straight chain alkyls include methyl, ethyl, n-propyl, n-butyl, n-pentyl, n-hexyl, and the like; while saturated branched alkyls include isopropyl, sec-butyl, isobutyl, tert-butyl, isopentyl, and the like. Representative saturated cyclic alkyls include cyclopropyl, cyclobutyl, cyclopentyl, cyclohexyl, and the like; while unsaturated cyclic alkyls include cyclopentenyl and cyclohexenyl, and the like.

"Alkenyl" means an alkyl, as defined above, containing at least one double bond between adjacent carbon atoms. Alkenyls include both cis and trans isomers. Representative straight chain and branched alkenyls include ethylenyl, propylenyl, 1-butenyl, 2-butenyl, isobutylenyl, 1-pentenyl, 2-pentenyl, 3-methyl-1-butenyl, 2-methyl-2-butenyl, 2,3-dimethyl-2-butenyl, and the like.

"Alkynyl" means any alkyl or alkenyl, as defined above, which additionally contains at least one triple bond between adjacent carbons. Representative straight chain and branched alkynyls include acetylenyl, propynyl, 1-butynyl, 2-butynyl, 1-pentynyl, 2-pentynyl, 3-methyl-1 butynyl, and the like.

"Acyl" means any alkyl, alkenyl, or alkynyl wherein the carbon at the point of attachment is substituted with an oxo group, as defined below. For example, —C(═O)alkyl, —C(═O)alkenyl, and —C(═O)alkynyl are acyl groups.

"Heterocycle" means a 5- to 7-membered monocyclic, or 7- to 10-membered bicyclic, heterocyclic ring which is either saturated, unsaturated, or aromatic, and which contains from 1 or 2 heteroatoms independently selected from nitrogen, oxygen and sulfur, and wherein the nitrogen and sulfur heteroatoms may be optionally oxidized, and the nitrogen heteroatom may be optionally quaternized, including bicyclic rings in which any of the above heterocycles are fused to a benzene ring. The heterocycle can be attached via any heteroatom or carbon atom. Heterocycles include heteroaryls as defined below. Heterocycles include morpholinyl, pyrrolidinonyl, pyrrolidinyl, piperidinyl, piperizynyl, hydantoinyl, valerolactamyl, oxiranyl, oxetanyl, tetrahydrofuranyl, tetrahydropyranyl, tetrahydropyridinyl, tetrahydroprimidinyl, tetrahydrothiophenyl, tetrahydrothiopyranyl, tetrahydropyrimidinyl, tetrahydrothiophenyl, tetrahydrothiopyranyl, and the like.

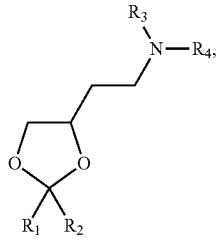
The terms "optionally substituted alkyl", "optionally substituted alkenyl", "optionally substituted alkynyl", "optionally substituted acyl", and "optionally substituted heterocycle" means that, when substituted, at least one hydrogen atom is replaced with a substituent. In the case of an oxo substituent (═O) two hydrogen atoms are replaced. In this regard, substituents include oxo, halogen, heterocycle, —CN, $—OR^x$, $—NR^xR^y$, $—NR^xC(═O)R^y$, $—NR^xSO_2R^y$, $—C(═O)R^x$, $—C(═O)OR^x$, $—C(═O)NR^xR^y$, $—SO_nR^x$ and $—SO_nNR^xR^y$, wherein n is 0, 1 or 2, R^x and R^y are the same or different and independently hydrogen, alkyl or heterocycle, and each of said alkyl and heterocycle substituents may be further substituted with one or more of oxo, halogen, —OH, —CN, alkyl, $—OR^x$, heterocycle, $—NR^xR^y$, $—NR^xC(═O)R^y$, $—NR^xSO_2R^y$, $—C(═O)R^x$, $—C(═O)OR^x$, $—C(═O)NR^xR^y$, $—SO_nR^x$ and $—SO_nNR^xR^y$.

"Halogen" means fluoro, chloro, bromo and iodo.

In some embodiments, the methods of the invention can require the use of protecting groups. Protecting group methodology is well known to those skilled in the art (see, for example, Protective Groups in Organic Synthesis, Green, T. W. et al., Wiley-Interscience, New York City, 1999). Briefly, protecting groups within the context of this invention are any group that reduces or eliminates unwanted reactivity of a functional group. A protecting group can be added to a functional group to mask its reactivity during certain reactions and then removed to reveal the original functional group. In some embodiments, an "alcohol protecting group" is used. An "alcohol protecting group" is any group which decreases or eliminates unwanted reactivity of an alcohol functional group. Protecting groups can be added and removed using techniques well known in the art.

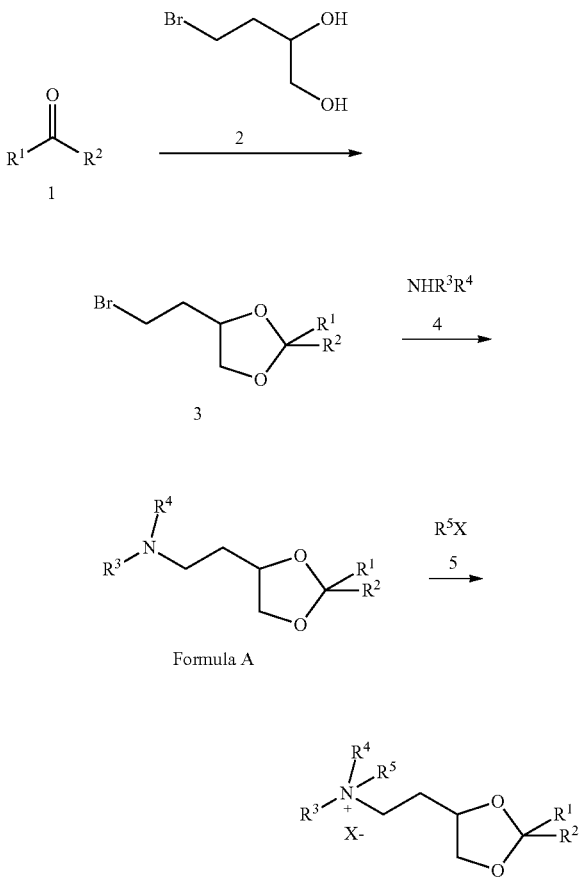
Synthesis of Formula A

In some embodiments, nucleic acid-lipid particles of the invention are formulated using a cationic lipid of formula A:



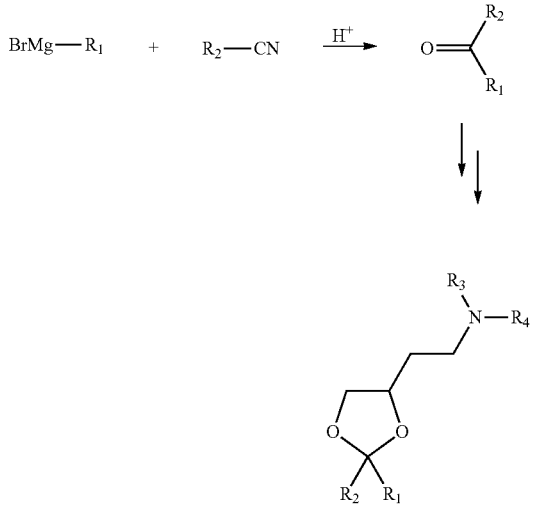
where R1 and R2 are independently alkyl, alkenyl or alkynyl, each can be optionally substituted, and R3 and R4 are independently lower alkyl or R3 and R4 can be taken together to form an optionally substituted heterocyclic ring. In some embodiments, the cationic lipid is XTC (2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane). In general, the lipid of formula A above may be made by the following Reaction Schemes 1 or 2, wherein all substituents are as defined above unless indicated otherwise.

Scheme 1



Lipid A, where R_1 and R_2 are independently alkyl, alkenyl or alkynyl, each can be optionally substituted, and R_3 and R_4 are independently lower alkyl or R_3 and R_4 can be taken together to form an optionally substituted heterocyclic ring, can be prepared according to Scheme 1. Ketone 1 and bromide 2 can be purchased or prepared according to methods known to those of ordinary skill in the art. Reaction of 1 and 2 yields ketal 3. Treatment of ketal 3 with amine 4 yields lipids of formula A. The lipids of formula A can be converted to the corresponding ammonium salt with an organic salt of formula 5, where X is anion counter ion selected from halogen, hydroxide, phosphate, sulfate, or the like.

Scheme 2



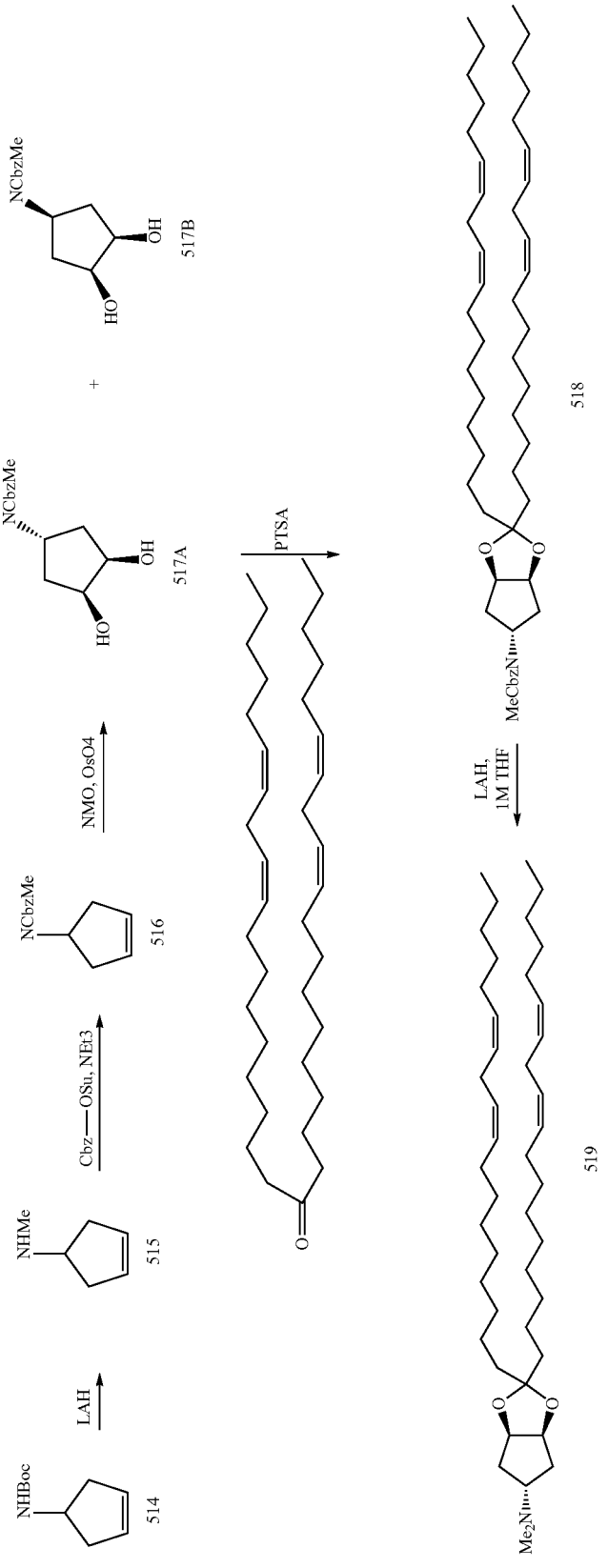
Alternatively, the ketone 1 starting material can be prepared according to Scheme 2. Grignard reagent 6 and cyanide 7 can be purchased or prepared according to methods known to those of ordinary skill in the art. Reaction of 6 and 7 yields ketone 1. Conversion of ketone 1 to the corresponding lipids of formula A is as described in Scheme 1.

Synthesis of MC3

Preparation of DLin-M-C3-DMA (i.e., (6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-yl 4-(dimethylamino) butanoate) was as follows. A solution of (6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-ol (0.53 g), 4-N,N-dimethylaminobutyric acid hydrochloride (0.51 g), 4-N,N-dimethylaminopyridine (0.61 g) and 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide hydrochloride (0.53 g) in dichloromethane (5 mL) was stirred at room temperature overnight. The solution was washed with dilute hydrochloric acid followed by dilute aqueous sodium bicarbonate. The organic fractions were dried over anhydrous magnesium sulphate, filtered and the solvent removed on a rotovap. The residue was passed down a silica gel column (20 g) using a 1-5% methanol/dichloromethane elution gradient. Fractions containing the purified product were combined and the solvent removed, yielding a colorless oil (0.54 g).

Synthesis of ALNY-100

Synthesis of ketal 519 [ALNY-100] was performed using the following scheme 3:


NHBoc
514
LAH
NHMe
515
Cbz—OSu, NEt3
NCbzMe
516
NMO, OsO4
NCbzMe
HO
OH
517A
+
NCbzMe
HO
OH
517B
PTSA
O
LAH,
1M THF
MeCbzN
518
Me2N
519

Synthesis of 515

To a stirred suspension of LiAlH4 (3.74 g, 0.09852 mol) in 200 ml anhydrous THF in a two neck RBF (1 L), was added a solution of 514 (10 g, 0.04926 mol) in 70 mL of THF slowly at 0° C. under nitrogen atmosphere. After complete addition, reaction mixture was warmed to room temperature and then heated to reflux for 4 h. Progress of the reaction was monitored by TLC. After completion of reaction (by TLC) the mixture was cooled to 0° C. and quenched with careful addition of saturated Na2SO4 solution. Reaction mixture was stirred for 4 h at room temperature and filtered off. Residue was washed well with THF. The filtrate and washings were mixed and diluted with 400 mL dioxane and 26 mL conc. HCl and stirred for 20 minutes at room temperature. The volatilities were stripped off under vacuum to furnish the hydrochloride salt of 515 as a white solid. Yield: 7.12 g 1H-NMR (DMSO, 400 MHz): δ=9.34 (broad, 2H), 5.68 (s, 2H), 3.74 (m, 1H), 2.66-2.60 (m, 2H), 2.50-2.45 (m, 5H).

Synthesis of 516

To a stirred solution of compound 515 in 100 mL dry DCM in a 250 mL two neck RBF, was added NEt3 (37.2 mL, 0.2669 mol) and cooled to 0° C. under nitrogen atmosphere. After a slow addition of N-(benzyloxy-carbonyloxy)-succinimide (20 g, 0.08007 mol) in 50 mL dry DCM, reaction mixture was allowed to warm to room temperature. After completion of the reaction (2-3 h by TLC) mixture was washed successively with 1N HCl solution (1×100 mL) and saturated NaHCO3 solution (1×50 mL). The organic layer was then dried over anhyd. Na2SO4 and the solvent was evaporated to give crude material which was purified by silica gel column chromatography to get 516 as sticky mass. Yield: 11 g (89%). 1H-NMR (CDCl3, 400 MHz): δ=7.36-7.27 (m, 5H), 5.69 (s, 2H), 5.12 (s, 2H), 4.96 (br., 1H) 2.74 (s, 3H), 2.60 (m, 2H), 2.30-2.25(m, 2H). LC-MS [M+H]-232.3 (96.94%).

Synthesis of 517A and 517B

The cyclopentene 516 (5 g, 0.02164 mol) was dissolved in a solution of 220 mL acetone and water (10:1) in a single neck 500 mL RBF and to it was added N-methyl morpholine-N-oxide (7.6 g, 0.06492 mol) followed by 4.2 mL of 7.6% solution of OsO4 (0.275 g, 0.00108 mol) in tert-butanol at room temperature. After completion of the reaction (~3 h), the mixture was quenched with addition of solid Na2SO3 and resulting mixture was stirred for 1.5 h at room temperature. Reaction mixture was diluted with DCM (300 mL) and washed with water (2×100 mL) followed by saturated NaHCO3 (1×50 mL) solution, water (1×30 mL) and finally with brine (1×50 mL). Organic phase was dried over an.Na2SO4 and solvent was removed in vacuum. Silica gel column chromatographic purification of the crude material was afforded a mixture of diastereomers, which were separated by prep HPLC. Yield: ~6 g crude

517A—Peak-1 (white solid), 5.13 g (96%). 1H-NMR (DMSO, 400 MHz): δ=7.39-7.31 (m, 5H), 5.04 (s, 2H), 4.78-4.73 (m, 1H), 4.48-4.47 (d, 2H), 3.94-3.93(m, 2H), 2.71 (s, 3H), 1.72-1.67 (m, 4H). LC-MS-[M+H]-266.3, [M+NH4+]-283.5 present, HPLC-97.86%. Stereochemistry confirmed by X-ray.

Synthesis of 518

Using a procedure analogous to that described for the synthesis of compound 505, compound 518 (1.2 g, 41%) was obtained as a colorless oil. 1H-NMR (CDCl3, 400 MHz): δ=7.35-7.33 (m, 4H), 7.30-7.27(m, 1H), 5.37-5.27(m, 8H), 5.12(s, 2H), 4.75(m,1H), 4.58-4.57(m,2H), 2.78-2.74(m, 7H), 2.06-2.00(m, 8H), 1.96-1.91(m, 2H), 1.62(m,4H), 1.48 (m,2H), 1.37-1.25(br m, 36H), 0.87 (m, 6H). HPLC-98.65%.

General Procedure for the Synthesis of Compound 519

A solution of compound 518 (1 eq) in hexane (15 mL) was added in a drop-wise fashion to an ice-cold solution of LAH in THF (1 M, 2 eq). After complete addition, the mixture was heated at 40° C. over 0.5 h then cooled again on an ice bath. The mixture was carefully hydrolyzed with saturated aqueous Na2SO4 then filtered through celite and reduced to an oil. Column chromatography provided the pure 519 (1.3 g, 68%) which was obtained as a colorless oil. 13C NMR □=130.2, 130.1 (x2), 127.9 (x3), 112.3, 79.3, 64.4, 44.7, 38.3, 35.4, 31.5, 29.9 (x2), 29.7, 29.6 (x2), 29.5 (x3), 29.3 (x2), 27.2 (x3), 25.6, 24.5, 23.3, 226, 14.1; Electrospray MS (+ve): Molecular weight for C44H80NO2 (M+H)+Calc. 654.6, Found 654.6.

Formulations prepared by either the standard or extrusion-free method can be characterized in similar manners. For example, formulations are typically characterized by visual inspection. They should be whitish translucent solutions free from aggregates or sediment. Particle size and particle size distribution of lipid-nanoparticles can be measured by light scattering using, for example, a Malvern Zetasizer Nano ZS (Malvern, USA). Particles should be about 20-300 nm, such as 40-100 nm in size. The particle size distribution should be unimodal. The total dsRNA concentration in the formulation, as well as the entrapped fraction, is estimated using a dye exclusion assay. A sample of the formulated dsRNA can be incubated with an RNA-binding dye, such as Ribogreen (Molecular Probes) in the presence or absence of a formulation disrupting surfactant, e.g., 0.5% Triton-X100. The total dsRNA in the formulation can be determined by the signal from the sample containing the surfactant, relative to a standard curve. The entrapped fraction is determined by subtracting the "free" dsRNA content (as measured by the signal in the absence of surfactant) from the total dsRNA content. Percent entrapped dsRNA is typically >85%. For SNALP formulation, the particle size is at least 30 nm, at least 40 nm, at least 50 nm, at least 60 nm, at least 70 nm, at least 80 nm, at least 90 nm, at least 100 nm, at least 110 nm, and at least 120 nm. The suitable range is typically about at least 50 nm to about at least 110 nm, about at least 60 nm to about at least 100 nm, or about at least 80 nm to about at least 90 nm.

Compositions and formulations for oral administration include powders or granules, microparticulates, nanoparticulates, suspensions or solutions in water or non-aqueous media, capsules, gel capsules, sachets, tablets or minitablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders may be desirable. In some embodiments, oral formulations are those in which dsRNAs featured in the invention are administered in conjunction with one or more penetration enhancers surfactants and chelators. Suitable surfactants include fatty acids and/or esters or salts thereof, bile acids and/or salts thereof. Suitable bile acids/salts include chenodeoxycholic acid (CDCA) and ursodeoxychenodeoxycholic acid (UDCA), cholic acid, dehydrocholic acid, deoxycholic acid, glucholic acid, glycholic acid, glycodeoxycholic acid, taurocholic acid, taurodeoxycholic acid, sodium tauro-24,25-dihydro-fusidate and sodium glycodihydrofusidate. Suitable fatty acids include arachidonic acid, undecanoic acid, oleic acid, lauric acid, caprylic acid, capric acid, myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein, dilaurin, glyceryl 1-monocaprate, 1-dodecylazacycloheptan-2-one, an acylcarnitine, an acylcholine, or a monoglyceride, a diglyceride or a pharmaceutically acceptable salt thereof (e.g., sodium). In some embodiments, combinations of penetration enhancers are used, for example, fatty acids/salts in combination with bile acids/salts. One exemplary combination is the sodium

salt of lauric acid, capric acid and UDCA. Further penetration enhancers include polyoxyethylene-9-lauryl ether, polyoxyethylene-20-cetyl ether. DsRNAs featured in the invention may be delivered orally, in granular form including sprayed dried particles, or complexed to form micro or nanoparticles. DsRNA complexing agents include poly-amino acids; polyimines; polyacrylates; polyalkylacrylates, polyoxethanes, polyalkylcyanoacrylates; cationized gelatins, albumins, starches, acrylates, polyethyleneglycols (PEG) and starches; polyalkylcyanoacrylates; DEAE-derivatized polyimines, pollulans, celluloses and starches. Suitable complexing agents include chitosan, N-trimethylchitosan, poly-L-lysine, polyhistidine, polyornithine, polyspermines, protamine, polyvinylpyridine, polythiodiethylaminomethylethylene P(TDAE), polyaminostyrene (e.g., p-amino), poly(methylcyanoacrylate), poly(ethylcyanoacrylate), poly(butylcyanoacrylate), poly(isobutylcyanoacrylate), poly(isohexylcynaoacrylate), DEAE-methacrylate, DEAE-hexylacrylate, DEAE-acrylamide, DEAE-albumin and DEAE-dextran, polymethylacrylate, polyhexylacrylate, poly(D,L-lactic acid), poly(DL-lactic-co-glycolic acid (PLGA), alginate, and polyethyleneglycol (PEG). Oral formulations for dsRNAs and their preparation are described in detail in U.S. Pat. No. 6,887,906, US Publn. No. 20030027780, and U.S. Pat. No. 6,747,014, each of which is incorporated herein by reference.

Compositions and formulations for parenteral, intraparenchymal (into the brain), intrathecal, intraventricular or intrahepatic administration may include sterile aqueous solutions which may also contain buffers, diluents and other suitable additives such as, but not limited to, penetration enhancers, carrier compounds and other pharmaceutically acceptable carriers or excipients.

Pharmaceutical compositions of the present invention include, but are not limited to, solutions, emulsions, and liposome-containing formulations. These compositions may be generated from a variety of components that include, but are not limited to, preformed liquids, self-emulsifying solids and self-emulsifying semisolids. Particularly preferred are formulations that target the liver when treating hepatic disorders such as hepatic carcinoma.

The pharmaceutical formulations of the present invention, which may conveniently be presented in unit dosage form, may be prepared according to conventional techniques well known in the pharmaceutical industry. Such techniques include the step of bringing into association the active ingredients with the pharmaceutical carrier(s) or excipient(s). In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredients with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

The compositions of the present invention may be formulated into any of many possible dosage forms such as, but not limited to, tablets, capsules, gel capsules, liquid syrups, soft gels, suppositories, and enemas. The compositions of the present invention may also be formulated as suspensions in aqueous, non-aqueous or mixed media. Aqueous suspensions may further contain substances which increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol and/or dextran. The suspension may also contain stabilizers.

Additional Formulations

Emulsions

The compositions of the present invention can be prepared and formulated as emulsions. Emulsions are typically heterogeneous systems of one liquid dispersed in another in the form of droplets usually exceeding 0.1 μm in diameter (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, L V., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, N.Y.; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199; Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., Volume 1, p. 245; Block in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 2, p. 335; Higuchi et al., in Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, Pa., 1985, p. 301). Emulsions are often biphasic systems comprising two immiscible liquid phases intimately mixed and dispersed with each other. In general, emulsions may be of either the water-in-oil (w/o) or the oil-in-water (o/w) variety. When an aqueous phase is finely divided into and dispersed as minute droplets into a bulk oily phase, the resulting composition is called a water-in-oil (w/o) emulsion. Alternatively, when an oily phase is finely divided into and dispersed as minute droplets into a bulk aqueous phase, the resulting composition is called an oil-in-water (o/w) emulsion. Emulsions may contain additional components in addition to the dispersed phases, and the active drug which may be present as a solution in either the aqueous phase, oily phase or itself as a separate phase. Pharmaceutical excipients such as emulsifiers, stabilizers, dyes, and anti-oxidants may also be present in emulsions as needed. Pharmaceutical emulsions may also be multiple emulsions that are comprised of more than two phases such as, for example, in the case of oil-in-water-in-oil (o/w/o) and water-in-oil-in-water (w/o/w) emulsions. Such complex formulations often provide certain advantages that simple binary emulsions do not. Multiple emulsions in which individual oil droplets of an o/w emulsion enclose small water droplets constitute a w/o/w emulsion. Likewise a system of oil droplets enclosed in globules of water stabilized in an oily continuous phase provides an o/w/o emulsion.

Emulsions are characterized by little or no thermodynamic stability. Often, the dispersed or discontinuous phase of the emulsion is well dispersed into the external or continuous phase and maintained in this form through the means of emulsifiers or the viscosity of the formulation. Either of the phases of the emulsion may be a semisolid or a solid, as is the case of emulsion-style ointment bases and creams. Other means of stabilizing emulsions entail the use of emulsifiers that may be incorporated into either phase of the emulsion. Emulsifiers may broadly be classified into four categories: synthetic surfactants, naturally occurring emulsifiers, absorption bases, and finely dispersed solids (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, L V., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, N.Y.; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).

Synthetic surfactants, also known as surface active agents, have found wide applicability in the formulation of emulsions and have been reviewed in the literature (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, L V., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, N.Y.; Rieger, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 285; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), Marcel Dekker, Inc., New York, N.Y., 1988, volume 1, p. 199). Surfactants are typically amphiphilic and comprise a hydrophilic and a hydrophobic portion. The ratio of the hydrophilic to the

hydrophobic nature of the surfactant has been termed the hydrophile/lipophile balance (HLB) and is a valuable tool in categorizing and selecting surfactants in the preparation of formulations. Surfactants may be classified into different classes based on the nature of the hydrophilic group: nonionic, anionic, cationic and amphoteric (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, L V., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, N.Y. Rieger, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 285).

Naturally occurring emulsifiers used in emulsion formulations include lanolin, beeswax, phosphatides, lecithin and acacia. Absorption bases possess hydrophilic properties such that they can soak up water to form w/o emulsions yet retain their semisolid consistencies, such as anhydrous lanolin and hydrophilic petrolatum. Finely divided solids have also been used as good emulsifiers especially in combination with surfactants and in viscous preparations. These include polar inorganic solids, such as heavy metal hydroxides, nonswelling clays such as bentonite, attapulgite, hectorite, kaolin, montmorillonite, colloidal aluminum silicate and colloidal magnesium aluminum silicate, pigments and nonpolar solids such as carbon or glyceryl tristearate.

A large variety of non-emulsifying materials are also included in emulsion formulations and contribute to the properties of emulsions. These include fats, oils, waxes, fatty acids, fatty alcohols, fatty esters, humectants, hydrophilic colloids, preservatives and antioxidants (Block, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 335; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).

Hydrophilic colloids or hydrocolloids include naturally occurring gums and synthetic polymers such as polysaccharides (for example, acacia, agar, alginic acid, carrageenan, guar gum, karaya gum, and tragacanth), cellulose derivatives (for example, carboxymethylcellulose and carboxypropylcellulose), and synthetic polymers (for example, carbomers, cellulose ethers, and carboxyvinyl polymers). These disperse or swell in water to form colloidal solutions that stabilize emulsions by forming strong interfacial films around the dispersed-phase droplets and by increasing the viscosity of the external phase.

Since emulsions often contain a number of ingredients such as carbohydrates, proteins, sterols and phosphatides that may readily support the growth of microbes, these formulations often incorporate preservatives. Commonly used preservatives included in emulsion formulations include methyl paraben, propyl paraben, quaternary ammonium salts, benzalkonium chloride, esters of p-hydroxybenzoic acid, and boric acid. Antioxidants are also commonly added to emulsion formulations to prevent deterioration of the formulation. Antioxidants used may be free radical scavengers such as tocopherols, alkyl gallates, butylated hydroxyanisole, butylated hydroxytoluene, or reducing agents such as ascorbic acid and sodium metabisulfite, and antioxidant synergists such as citric acid, tartaric acid, and lecithin.

The application of emulsion formulations via dermatological, oral and parenteral routes and methods for their manufacture have been reviewed in the literature (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, L V., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, N.Y.; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199). Emulsion formulations for oral delivery have been very widely used because of ease of formulation, as well as efficacy from an absorption and bioavailability standpoint (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, L V., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, N.Y.; Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199). Mineral-oil base laxatives, oil-soluble vitamins and high fat nutritive preparations are among the materials that have commonly been administered orally as o/w emulsions.

In one embodiment of the present invention, the compositions of iRNAs and nucleic acids are formulated as microemulsions. A microemulsion may be defined as a system of water, oil and amphiphile which is a single optically isotropic and thermodynamically stable liquid solution (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, L V., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, N.Y.; Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245). Typically microemulsions are systems that are prepared by first dispersing an oil in an aqueous surfactant solution and then adding a sufficient amount of a fourth component, generally an intermediate chain-length alcohol to form a transparent system. Therefore, microemulsions have also been described as thermodynamically stable, isotropically clear dispersions of two immiscible liquids that are stabilized by interfacial films of surface-active molecules (Leung and Shah, in: Controlled Release of Drugs: Polymers and Aggregate Systems, Rosoff, M., Ed., 1989, VCH Publishers, New York, pages 185-215). Microemulsions commonly are prepared via a combination of three to five components that include oil, water, surfactant, cosurfactant and electrolyte. Whether the microemulsion is of the water-in-oil (w/o) or an oil-in-water (o/w) type is dependent on the properties of the oil and surfactant used and on the structure and geometric packing of the polar heads and hydrocarbon tails of the surfactant molecules (Schott, in Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, Pa., 1985, p. 271).

The phenomenological approach utilizing phase diagrams has been extensively studied and has yielded a comprehensive knowledge, to one skilled in the art, of how to formulate microemulsions (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, L V., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, N.Y.; Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245; Block, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 335). Compared to conventional emulsions, microemulsions offer the advantage of solubilizing water-insoluble drugs in a formulation of thermodynamically stable droplets that are formed spontaneously.

Surfactants used in the preparation of microemulsions include, but are not limited to, ionic surfactants, non-ionic surfactants, Brij 96, polyoxyethylene oleyl ethers, polyglycerol fatty acid esters, tetraglycerol monolaurate (ML310), tetraglycerol monooleate (MO310), hexaglycerol monooleate (PO310), hexaglycerol pentaoleate (PO500), decaglycerol monocaprate (MCA750), decaglycerol monooleate (MO750), decaglycerol sequioleate (SO750),

decaglycerol decaoleate (DAO750), alone or in combination with cosurfactants. The cosurfactant, usually a short-chain alcohol such as ethanol, 1-propanol, and 1-butanol, serves to increase the interfacial fluidity by penetrating into the surfactant film and consequently creating a disordered film because of the void space generated among surfactant molecules. Microemulsions may, however, be prepared without the use of cosurfactants and alcohol-free self-emulsifying microemulsion systems are known in the art. The aqueous phase may typically be, but is not limited to, water, an aqueous solution of the drug, glycerol, PEG300, PEG400, polyglycerols, propylene glycols, and derivatives of ethylene glycol. The oil phase may include, but is not limited to, materials such as Captex 300, Captex 355, Capmul MCM, fatty acid esters, medium chain (C8-C12) mono, di, and tri-glycerides, polyoxyethylated glyceryl fatty acid esters, fatty alcohols, polyglycolized glycerides, saturated polyglycolized C8-C10 glycerides, vegetable oils and silicone oil.

Microemulsions are particularly of interest from the standpoint of drug solubilization and the enhanced absorption of drugs. Lipid based microemulsions (both o/w and w/o) have been proposed to enhance the oral bioavailability of drugs, including peptides (see e.g., U.S. Pat. Nos. 6,191,105; 7,063,860; 7,070,802; 7,157,099; Constantinides et al., Pharmaceutical Research, 1994, 11, 1385-1390; Ritschel, Meth. Find. Exp. Clin. Pharmacol., 1993, 13, 205). Microemulsions afford advantages of improved drug solubilization, protection of drug from enzymatic hydrolysis, possible enhancement of drug absorption due to surfactant-induced alterations in membrane fluidity and permeability, ease of preparation, ease of oral administration over solid dosage forms, improved clinical potency, and decreased toxicity (see e.g., U.S. Pat. Nos. 6,191,105; 7,063,860; 7,070,802; 7,157,099; Constantinides et al., Pharmaceutical Research, 1994, 11, 1385; Ho et al., J. Pharm. Sci., 1996, 85, 138-143). Often microemulsions may form spontaneously when their components are brought together at ambient temperature. This may be particularly advantageous when formulating thermolabile drugs, peptides or iRNAs. Microemulsions have also been effective in the transdermal delivery of active components in both cosmetic and pharmaceutical applications. It is expected that the microemulsion compositions and formulations of the present invention will facilitate the increased systemic absorption of iRNAs and nucleic acids from the gastrointestinal tract, as well as improve the local cellular uptake of iRNAs and nucleic acids.

Microemulsions of the present invention may also contain additional components and additives such as sorbitan monostearate (Grill 3), Labrasol, and penetration enhancers to improve the properties of the formulation and to enhance the absorption of the iRNAs and nucleic acids of the present invention. Penetration enhancers used in the microemulsions of the present invention may be classified as belonging to one of five broad categories—surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants (Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, p. 92). Each of these classes has been discussed above.

Penetration Enhancers

In one embodiment, the present invention employs various penetration enhancers to effect the efficient delivery of nucleic acids, particularly iRNAs, to the skin of animals. Most drugs are present in solution in both ionized and non-ionized forms. However, usually only lipid soluble or lipophilic drugs readily cross cell membranes. It has been discovered that even non-lipophilic drugs may cross cell membranes if the membrane to be crossed is treated with a penetration enhancer. In addition to aiding the diffusion of non-lipophilic drugs across cell membranes, penetration enhancers also enhance the permeability of lipophilic drugs.

Penetration enhancers may be classified as belonging to one of five broad categories, i.e., surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants (see e.g., Malmsten, M. Surfactants and polymers in drug delivery, Informa Health Care, New York, N.Y., 2002; Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, p. 92). Each of the above mentioned classes of penetration enhancers are described below in greater detail.

Surfactants: In connection with the present invention, surfactants (or "surface-active agents") are chemical entities which, when dissolved in an aqueous solution, reduce the surface tension of the solution or the interfacial tension between the aqueous solution and another liquid, with the result that absorption of iRNAs through the mucosa is enhanced. In addition to bile salts and fatty acids, these penetration enhancers include, for example, sodium lauryl sulfate, polyoxyethylene-9-lauryl ether and polyoxyethylene-20-cetyl ether) (see e.g., Malmsten, M. Surfactants and polymers in drug delivery, Informa Health Care, New York, N.Y., 2002; Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, p. 92); and perfluorochemical emulsions, such as FC-43. Takahashi et al., J. Pharm. Pharmacol., 1988, 40, 252).

Fatty acids: Various fatty acids and their derivatives which act as penetration enhancers include, for example, oleic acid, lauric acid, capric acid (n-decanoic acid), myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein (1-monooleoyl-rac-glycerol), dilaurin, caprylic acid, arachidonic acid, glycerol 1-monocaprate, 1-dodecylazacycloheptan-2-one, acylcarnitines, acylcholines, C_{1-20} alkyl esters thereof (e.g., methyl, isopropyl and t-butyl), and mono- and di-glycerides thereof (i.e., oleate, laurate, caprate, myristate, palmitate, stearate, linoleate, etc.) (see e.g., Touitou, E., et al. Enhancement in Drug Delivery, CRC Press, Danvers, Mass., 2006; Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, p. 92; Muranishi, Critical Reviews in Therapeutic Drug Carrier Systems, 1990, 7, 1-33; El Hariri et al., J. Pharm. Pharmacol., 1992, 44, 651-654).

Bile salts: The physiological role of bile includes the facilitation of dispersion and absorption of lipids and fat-soluble vitamins (see e.g., Malmsten, M. Surfactants and polymers in drug delivery, Informa Health Care, New York, N.Y., 2002; Brunton, Chapter 38 in: Goodman & Gilman's The Pharmacological Basis of Therapeutics, 9th Ed., Hardman et al. Eds., McGraw-Hill, New York, 1996, pp. 934-935). Various natural bile salts, and their synthetic derivatives, act as penetration enhancers. Thus the term "bile salts" includes any of the naturally occurring components of bile as well as any of their synthetic derivatives. Suitable bile salts include, for example, cholic acid (or its pharmaceutically acceptable sodium salt, sodium cholate), dehydrocholic acid (sodium dehydrocholate), deoxycholic acid (sodium deoxycholate), glucholic acid (sodium glucholate), glycholic acid (sodium glycocholate), glycodeoxycholic acid (sodium glycodeoxycholate), taurocholic acid (sodium taurocholate), taurodeoxycholic acid (sodium taurodeoxycholate), chenodeoxycholic acid (sodium chenodeoxycholate), ursodeoxycholic acid (UDCA), sodium tauro-24,25-dihydro-fusidate (STDHF), sodium glycodihydrofusidate and polyoxyethylene-9-lauryl ether (POE) (see e.g., Malmsten, M. Surfactants and polymers in drug delivery, Informa Health Care, New York, N.Y., 2002; Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, page 92; Swinyard, Chapter 39 In: Remington's Pharmaceutical Sciences, 18th Ed., Gennaro, ed., Mack

Publishing Co., Easton, Pa., 1990, pages 782-783; Muranishi, Critical Reviews in Therapeutic Drug Carrier Systems, 1990, 7, 1-33; Yamamoto et al., J. Pharm. Exp. Ther., 1992, 263, 25; Yamashita et al., J. Pharm. Sci., 1990, 79, 579-583).

Chelating Agents: Chelating agents, as used in connection with the present invention, can be defined as compounds that remove metallic ions from solution by forming complexes therewith, with the result that absorption of iRNAs through the mucosa is enhanced. With regards to their use as penetration enhancers in the present invention, chelating agents have the added advantage of also serving as DNase inhibitors, as most characterized DNA nucleases require a divalent metal ion for catalysis and are thus inhibited by chelating agents (Jarrett, J. Chromatogr., 1993, 618, 315-339). Suitable chelating agents include but are not limited to disodium ethylenediaminetetraacetate (EDTA), citric acid, salicylates (e.g., sodium salicylate, 5-methoxysalicylate and homovanilate), N-acyl derivatives of collagen, laureth-9 and N-amino acyl derivatives of beta-diketones (enamines)(see e.g., Katdare, A. et al., Excipient development for pharmaceutical, biotechnology, and drug delivery, CRC Press, Danvers, Mass., 2006; Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, page 92; Muranishi, Critical Reviews in Therapeutic Drug Carrier Systems, 1990, 7, 1-33; Buur et al., J. Control Rel., 1990, 14, 43-51).

Non-chelating non-surfactants: As used herein, non-chelating non-surfactant penetration enhancing compounds can be defined as compounds that demonstrate insignificant activity as chelating agents or as surfactants but that nonetheless enhance absorption of iRNAs through the alimentary mucosa (see e.g., Muranishi, Critical Reviews in Therapeutic Drug Carrier Systems, 1990, 7, 1-33). This class of penetration enhancers includes, for example, unsaturated cyclic ureas, 1-alkyl- and 1-alkenylazacyclo-alkanone derivatives (Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, page 92); and non-steroidal anti-inflammatory agents such as diclofenac sodium, indomethacin and phenylbutazone (Yamashita et al., J. Pharm. Pharmacol., 1987, 39, 621-626).

Agents that enhance uptake of iRNAs at the cellular level may also be added to the pharmaceutical and other compositions of the present invention. For example, cationic lipids, such as lipofectin (Junichi et al, U.S. Pat. No. 5,705,188), cationic glycerol derivatives, and polycationic molecules, such as polylysine (Lollo et al., PCT Application WO 97/30731), are also known to enhance the cellular uptake of dsRNAs. Examples of commercially available transfection reagents include, for example Lipofectamine™ (Invitrogen; Carlsbad, Calif.), Lipofectamine 2000™ (Invitrogen; Carlsbad, Calif.), 293Fectin™ (Invitrogen; Carlsbad, Calif.), Cellffectin™ (Invitrogen; Carlsbad, Calif.), DMRIE-C™ (Invitrogen; Carlsbad, Calif.), FreeStyle™ MAX (Invitrogen; Carlsbad, Calif.), Lipofectamine™ 2000 CD (Invitrogen; Carlsbad, Calif.), Lipofectamine™ (Invitrogen; Carlsbad, Calif.), RNAiMAX (Invitrogen; Carlsbad, Calif.), Oligofectamine™ (Invitrogen; Carlsbad, Calif.), Optifect™ (Invitrogen; Carlsbad, Calif.), X-tremeGENE Q2 Transfection Reagent (Roche; Grenzacherstrasse, Switzerland), DOTAP Liposomal Transfection Reagent (Grenzacherstrasse, Switzerland), DOSPER Liposomal Transfection Reagent (Grenzacherstrasse, Switzerland), or Fugene (Grenzacherstrasse, Switzerland), Transfectam® Reagent (Promega; Madison, Wis.), TransFast™ Transfection Reagent (Promega; Madison, Wis.), Tfx™-20 Reagent (Promega; Madison, Wis.), Tfx™-50 Reagent (Promega; Madison, Wis.), DreamFect™ (OZ Biosciences; Marseille, France), EcoTransfect (OZ Biosciences; Marseille, France), TransPass^a D1 Transfection Reagent (New England Biolabs; Ipswich, Mass., USA), LyoVec™/LipoGen™ (Invivogen; San Diego, Calif., USA), PerFectin Transfection Reagent (Genlantis; San Diego, Calif., USA), NeuroPORTER Transfection Reagent (Genlantis; San Diego, Calif., USA), GenePORTER Transfection reagent (Genlantis; San Diego, Calif., USA), GenePORTER 2 Transfection reagent (Genlantis; San Diego, Calif., USA), Cytofectin Transfection Reagent (Genlantis; San Diego, Calif., USA), BaculoPORTER Transfection Reagent (Genlantis; San Diego, Calif., USA), TroganPORTER™ transfection Reagent (Genlantis; San Diego, Calif., USA), RiboFect (Bioline; Taunton, Mass., USA), PlasFect (Bioline; Taunton, Mass., USA), UniFECTOR (B-Bridge International; Mountain View, Calif., USA), SureFECTOR (B-Bridge International; Mountain View, Calif., USA), or HiFect™ (B-Bridge International, Mountain View, Calif., USA), among others.

Other agents may be utilized to enhance the penetration of the administered nucleic acids, including glycols such as ethylene glycol and propylene glycol, pyrrols such as 2-pyrrol, azones, and terpenes such as limonene and menthone.

Carriers

Certain compositions of the present invention also incorporate carrier compounds in the formulation. As used herein, "carrier compound" or "carrier" can refer to a nucleic acid, or analog thereof, which is inert (i.e., does not possess biological activity per se) but is recognized as a nucleic acid by in vivo processes that reduce the bioavailability of a nucleic acid having biological activity by, for example, degrading the biologically active nucleic acid or promoting its removal from circulation. The coadministration of a nucleic acid and a carrier compound, typically with an excess of the latter substance, can result in a substantial reduction of the amount of nucleic acid recovered in the liver, kidney or other extracirculatory reservoirs, presumably due to competition between the carrier compound and the nucleic acid for a common receptor. For example, the recovery of a partially phosphorothioate dsRNA in hepatic tissue can be reduced when it is coadministered with polyinosinic acid, dextran sulfate, polycytidic acid or 4-acetamido-4'isothiocyano-stilbene-2,2'-disulfonic acid (Miyao et al., DsRNA Res. Dev., 1995, 5, 115-121; Takakura et al., DsRNA & Nucl. Acid Drug Dev., 1996, 6, 177-183.

Excipients

In contrast to a carrier compound, a "pharmaceutical carrier" or "excipient" is a pharmaceutically acceptable solvent, suspending agent or any other pharmacologically inert vehicle for delivering one or more nucleic acids to an animal. The excipient may be liquid or solid and is selected, with the planned manner of administration in mind, so as to provide for the desired bulk, consistency, etc., when combined with a nucleic acid and the other components of a given pharmaceutical composition. Typical pharmaceutical carriers include, but are not limited to, binding agents (e.g., pregelatinized maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose, etc.); fillers (e.g., lactose and other sugars, microcrystalline cellulose, pectin, gelatin, calcium sulfate, ethyl cellulose, polyacrylates or calcium hydrogen phosphate, etc.); lubricants (e.g., magnesium stearate, talc, silica, colloidal silicon dioxide, stearic acid, metallic stearates, hydrogenated vegetable oils, corn starch, polyethylene glycols, sodium benzoate, sodium acetate, etc.); disintegrants (e.g., starch, sodium starch glycolate, etc.); and wetting agents (e.g., sodium lauryl sulphate, etc).

Pharmaceutically acceptable organic or inorganic excipients suitable for non-parenteral administration which do not deleteriously react with nucleic acids can also be used to formulate the compositions of the present invention. Suitable

pharmaceutically acceptable carriers include, but are not limited to, water, salt solutions, alcohols, polyethylene glycols, gelatin, lactose, amylose, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose, polyvinylpyrrolidone and the like.

Formulations for topical administration of nucleic acids may include sterile and non-sterile aqueous solutions, non-aqueous solutions in common solvents such as alcohols, or solutions of the nucleic acids in liquid or solid oil bases. The solutions may also contain buffers, diluents and other suitable additives. Pharmaceutically acceptable organic or inorganic excipients suitable for non-parenteral administration which do not deleteriously react with nucleic acids can be used.

Suitable pharmaceutically acceptable excipients include, but are not limited to, water, salt solutions, alcohol, polyethylene glycols, gelatin, lactose, amylose, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose, polyvinylpyrrolidone and the like.

Other Components

The compositions of the present invention may additionally contain other adjunct components conventionally found in pharmaceutical compositions, at their art-established usage levels. Thus, for example, the compositions may contain additional, compatible, pharmaceutically-active materials such as, for example, antipruritics, astringents, local anesthetics or anti-inflammatory agents, or may contain additional materials useful in physically formulating various dosage forms of the compositions of the present invention, such as dyes, flavoring agents, preservatives, antioxidants, opacifiers, thickening agents and stabilizers. However, such materials, when added, should not unduly interfere with the biological activities of the components of the compositions of the present invention. The formulations can be sterilized and, if desired, mixed with auxiliary agents, e.g., lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, colorings, flavorings and/or aromatic substances and the like which do not deleteriously interact with the nucleic acid(s) of the formulation.

Aqueous suspensions can contain substances that increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol and/or dextran. The suspension may also contain stabilizers.

In some embodiments, pharmaceutical compositions featured in the invention include (a) one or more iRNA compounds and (b) one or more anti-cytokine biologic agents which function by a non-RNAi mechanism. Examples of such biologics include, biologics that target IL1β (e.g., anakinra), IL6 (e.g., tocilizumab), or TNF (e.g., etanercept, infliximab, adlimumab, or certolizumab).

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD50/ED50. Compounds that exhibit high therapeutic indices are preferred.

The data obtained from cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of compositions featured herein lies generally within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage can vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the methods featured in the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range of the compound or, when appropriate, of the polypeptide product of a target sequence (e.g., achieving a decreased concentration of the polypeptide) that includes the IC50 (i.e., the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

In addition to their administration, as discussed above, the iRNAs described herein can be administered in combination with other known agents effective in treatment of pathological processes mediated by Mylip/Idol expression. In any event, the administering physician can adjust the amount and timing of iRNA administration on the basis of results observed using standard measures of efficacy known in the art or described herein.

Methods for Treating Diseases Caused by Expression of a Mylip/Idol Gene

The invention relates in particular to the use of an iRNA targeting Mylip/Idol and compositions containing at least one such iRNA for the treatment of a Mylip/Idol-mediated disorder or disease. For example, a composition containing an iRNA targeting a Mylip/Idol gene is used for treatment of lipid or metabolic disorders, such as hypercholesterolemia, dyslipidemia, diabetes, diabetes type I, diabetes type II, coronary artery disease, atherosclerosis, myocardial infarction, coronary artery bypass graft, percutaneous transluminal angioplasties, coronary stenosis, cerebrovascular disease transient ischemic attack, ischemic stroke, carotid endarterectomies, peripheral arterial disease, and other disorders associated with cholesterol metabolism.

The invention further relates to the use of an iRNA or a pharmaceutical composition thereof, e.g., for treating a lipid disorder, in combination with other pharmaceuticals and/or other therapeutic methods, e.g., with known pharmaceuticals and/or known therapeutic methods, such as, for example, those which are currently employed for treating these disorders. For example, in certain embodiments, an iRNA targeting Mylip/Idol is administered in combination with, e.g., an HMG-CoA reductase inhibitor (e.g., a statin, such as atrovastatin, lovastatin, pravastatin or simvastatin), a fibrate, a bile acid sequestrant, niacin, an antiplatelet agent, an angiotensin converting enzyme inhibitor, an angiotensin II receptor antagonist (e.g., losartan potassium, such as Merck & Co.'s Cozaar®), an acylCoA cholesterol acetyltransferase (ACAT) inhibitor, a cholesterol absorption inhibitor, a cholesterol ester transfer protein (CETP) inhibitor, a microsomal triglyceride transfer protein (MTTP) inhibitor, a cholesterol modulator, a bile acid modulator, a peroxisome proliferation activated receptor (PPAR) agonist, a gene-based therapy, a composite vascular protectant (e.g., AGI-1067, from Atherogenics), a glycoprotein IIb/IIIa inhibitor, aspirin or an aspirin-like compound, an IBAT inhibitor (e.g., S-8921, from Shionogi), a squalene synthase inhibitor, or a monocyte chemoattractant protein (MCP)-I inhibitor. Exemplary HMG-CoA reductase inhibitors include atorvastatin (Pfizer's Lipitor®/Tahor/Sortis/Torvast/Cardyl), pravastatin (Bristol-Myers Squibb's Pravachol, Sankyo's Mevalotin/Sanaprav), simvastatin (Merck's Zocor®/Sinvacor, Boehringer Ingelheim's Denan, Banyu's Lipovas), lovastatin (Merck's Mevacor/Mevinacor, Bexal's Lovastatina, Cepa; Schwarz Pharma's Liposcler), fluvastatin (Novartis' Lescol®/Locol/Lochol, Fujisawa's Cranoc, Solvay's Digaril), cerivastatin (Bayer's Lipobay/GlaxoSmithKline's Baycol), rosuvastatin (AstraZeneca's Crestor®), and pitivastatin (itavastatin/risiv-

astatin) (Nissan Chemical, Kowa Kogyo, Sankyo, and Novartis). Exemplary fibrates include, e.g., bezafibrate (e.g., Roche's Befizal®/Cedur®/Bezalip®, Kissei's Bezatol), clofibrate (e.g., Wyeth's Atromid-S®), fenofibrate (e.g., Fournier's Lipidil/Lipantil, Abbott's Tricor®, Takeda's Lipantil, generics), gemfibrozil (e.g., Pfizer's Lopid/Lipur) and ciprofibrate (Sanofi-Synthelabo's Modalim®). Exemplary bile acid sequestrants include, e.g., cholestyramine (Bristol-Myers Squibb's Questran® and Questran Light™), colestipol (e.g., Pharmacia's Colestid), and colesevelam (Genzyme/Sankyo's WelChol™). Exemplary niacin therapies include, e.g., immediate release formulations, such as Aventis' Nicobid, Upsher-Smith's Niacor, Aventis' Nicolar, and Sanwakagaku's Perycit. Niacin extended release formulations include, e.g., Kos Pharmaceuticals' Niaspan and Upsher-Smith's SIo-Niacin. Exemplary antiplatelet agents include, e.g., aspirin (e.g., Bayer's aspirin), clopidogrel (Sanofi-Synthelabo/Bristol-Myers Squibb's Plavix), and ticlopidine (e.g., Sanofi-Synthelabo's Ticlid and Daiichi's Panaldine). Other aspirin-like compounds useful in combination with an iRNA targeting Mylip/Idol include, e.g., Asacard (slow-release aspirin, by Pharmacia) and Pamicogrel (Kanebo/Angelini Ricerche/CEPA). Exemplary angiotensin-converting enzyme inhibitors include, e.g., ramipril (e.g., Aventis' Altace) and enalapril (e.g., Merck & Co.'s Vasotec). Exemplary acyl CoA cholesterol acetyltransferase (ACAT) inhibitors include, e.g., avasimibe (Pfizer), eflucimibe (BioMєrieux Pierre Fabre/Eli Lilly), CS-505 (Sankyo and Kyoto), and SMP-797 (Sumito). Exemplary cholesterol absorption inhibitors include, e.g., ezetimibe (Merck/Schering-Plough Pharmaceuticals Zetia®) and Pamaqueside (Pfizer). Exemplary CETP inhibitors include, e.g., Torcetrapib (also called CP-529414, Pfizer), JTT-705 (Japan Tobacco), and CETi-I (Avant Immunotherapeutics). Exemplary microsomal triglyceride transfer protein (MTTP) inhibitors include, e.g., implitapide (Bayer), R-103757 (Janssen), and CP-346086 (Pfizer). Other exemplary cholesterol modulators include, e.g., NO-1886 (Otsuka/TAP Pharmaceutical), CI-1027 (Pfizer), and WAY-135433 (Wyeth-Ayerst). Exemplary bile acid modulators include, e.g., HBS-107 (Hisamitsu/Banyu), Btg-511 (British Technology Group), BARI-1453 (Aventis), S-8921 (Shionogi), SD-5613 (Pfizer), and AZD-7806 (AstraZeneca). Exemplary peroxisome proliferation activated receptor (PPAR) agonists include, e.g., tesaglitazar (AZ-242) (AstraZeneca), Netoglitazone (MCC-555) (Mitsubishi/Johnson & Johnson), GW-409544 (Ligand Pharmaceuticals/GlaxoSmithKline), GW-501516 (Ligand Pharmaceuticals/GlaxoSmithKline), LY-929 (Ligand Pharmaceuticals and Eli Lilly), LY-465608 (Ligand Pharmaceuticals and Eli Lilly), LY-518674 (Ligand Pharmaceuticals and Eli Lilly), and MK-767 (Merck and Kyorin). Exemplary gene-based therapies include, e.g., AdGWEGF121.10 (GenVec), ApoAl (UCB Pharma/Groupe Fournier), EG-004 (Trinam) (Ark Therapeutics), and ATP-binding cassette transporter-Al (ABCAl) (CV Therapeutics/Incyte, Aventis, Xenon). Exemplary Glycoprotein IIb/IIIa inhibitors include, e.g., roxifiban (also called DMP754, Bristol-Myers Squibb), Gantofiban (Merck KGaA/Yamanouchi), and Cromafiban (Millennium Pharmaceuticals). Exemplary squalene synthase inhibitors include, e.g., BMS-1884941 (Bristol-Myers Squibb), CP-210172 (Pfizer), CP-295697 (Pfizer), CP-294838 (Pfizer), and TAK-475 (Takeda). An exemplary MCP-I inhibitor is, e.g., RS-504393 (Roche Bioscience). The anti-atherosclerotic agent BO-653 (Chugai Pharmaceuticals), and the nicotinic acid derivative Nyclin (Yamanouchi Pharmaceuticals) are also appropriate for administering in combination with an iRNA featured in the invention. Exemplary combination therapies suitable for administration with an iRNA targeting Mylip/Idol include, e.g., advicor (Niacin/lovastatin from Kos Pharmaceuticals), amlodipine/atorvastatin (Pfizer), and ezetimibe/simvastatin (e.g., Vytorin® 10/10, 10/20, 10/40, and 10/80 tablets by Merck/Schering-Plough Pharmaceuticals). Agents for treating hypercholesterolemia, and suitable for administration in combination with an iRNA targeting Mylip/Idol include, e.g., lovastatin, niacin Altoprev® Extended-Release Tablets (Andrx Labs), lovastatin Caduet® Tablets (Pfizer), amlodipine besylate, atorvastatin calcium Crestor® Tablets (AstraZeneca), rosuvastatin calcium Lescol® Capsules (Novartis), fluvastatin sodium Lescol® (Reliant, Novartis), fluvastatin sodium Lipitor® Tablets (Parke-Davis), atorvastatin calcium Lofibra® Capsules (Gate), Niaspan Extended-Release Tablets (Kos), niacin Pravachol Tablets (Bristol-Myers Squibb), pravastatin sodium TriCor® Tablets (Abbott), fenofibrate Vytorin® 10/10 Tablets (Merck/Schering-Plough Pharmaceuticals), ezetimibe, simvastatin WelChol™ Tablets (Sankyo), colesevelam hydrochloride Zetia® Tablets (Schering), ezetimibe Zetia® Tablets (Merck/Schering-Plough Pharmaceuticals), and ezetimibe Zocor® Tablets (Merck).

In one embodiment, a dsRNA targeting Mylip/Idol is administered in combination with an ezetimibe/simvastatin combination (e.g., Vytorin® (Merck/Schering-Plough Pharmaceuticals)).

The invention further relates to the use of a dsRNA or a pharmaceutical composition containing a dsRNA for treatment of a metabolic disorder, such as diabetes, in combination with other pharmaceuticals and/or other therapeutic methods, e.g., with known pharmaceuticals and/or known therapeutic methods, such as, for example, those which are currently employed for treating metabolic disorders (e.g., diabetes). For example, in certain embodiments, administration of a dsRNA targeting Mylip/Idol is administered in combination with, e.g., insulin (e.g., insulin injections); a biguanide (e.g., metformin); a sulfonylurea (e.g., glibenclamide, glipizide, tolbautamide, chloropamidem, tolazamide, glimepride, glicazide or glyburide); an alpha-glucosidase inhibitor (e.g., acarbose); a PPAR gamma agonist (e.g., thiazolidinedione and derivatives such as rosiglitazone or pioglitazone); an oxadiazolidinedione; a meglitinide; a D-phenylalanine derivative; repaglinide; a PPAR (Peroxisome proliferator-activated receptor) ligand including the PPAR-alpha, PPAR-gamma and PPAR-delta subtypes; an RXR (retinoid X receptor) agonist, such as ALRT-268, LG-1268 or LG-1069; a PPAR alpha agonist (e.g., clofibrate and gemfibrozil); an alpha agonist (non-thiazolinedione); a glycogen phosphorylase inhibitor; a glucagon-like peptide; a dipeptidylpeptidase IV inhibitor; an HMG-CoA reductase inhibitor (e.g., a statin, such as atrovastatin, lovastatin, pravastatin or simvastatin); a GLP-1 antagonist; a DPP-IV (dipeptidyl peptidase-IV) inhibitor; a PTPase (protein tyrosine phosphatase) inhibitor; or a compound lowering food intake.

The iRNA and an additional therapeutic agent can be administered in the same combination, e.g., parenterally, or the additional therapeutic agent can be administered as part of a separate composition or by another method described herein.

The invention features a method of administering an iRNA agent targeting Mylip/Idol to a patient having a disease or disorder mediated by Mylip/Idol expression, such as a lipid disorder, or a disorder associated with cholesterol metabolism, e.g., diabetes or atherosclerosis. Administration of the dsRNA can lower LDL levels, lower ApoB levels, or lower total cholesterol level, for example, in a patient with a lipid disorder, or a disorder associated with cholesterol metabo-

lism. By "lower" in this context is meant a statistically significant decrease in such level. The decrease can be, for example, at least 10%, at least 20%, at least 30%, at least 40% or more, and is preferably down to a level accepted as within the range of normal for an individual without such disorder.

Efficacy of treatment or prevention of disease can be assessed, for example by measuring disease progression, disease remission, symptom severity, reduction in pain, quality of life, dose of a medication required to sustain a treatment effect, level of a disease marker or any other measurable parameter appropriate for a given disease being treated or targeted for prevention. It is well within the ability of one skilled in the art to monitor efficacy of treatment or prevention by measuring any one of such parameters, or any combination of parameters. For example, the levels of LDL cholesterol can be monitored for efficacy of a given treatment regime. The iRNA treatments described herein can be used to treat individuals having moderately elevated plasma LDL cholesterol levels (e.g., 130-159 mg/dL), high LDL plasma levels (e.g., 160-189 mg/dL), or very high LDL cholesterol levels (e.g., 190 mg/dL). In addition, the treatment described herein may also be used to prevent high LDL cholesterol levels in individuals with only minor elevations in LDL cholesterol (e.g., 100-129 mg/dL). One of skill in the art can easily monitor the LDL levels in subjects receiving treatment with iRNA as described herein and assay for a reduction in LDL cholesterol levels of at least 10% and preferably to a clinical level representing a low risk of LDL cholesterol mediated disease e.g., <100 mg/dL.

A treatment or preventive effect is evident when there is a statistically significant improvement in one or more parameters of disease status, or by a failure to worsen or to develop symptoms where they would otherwise be anticipated. As an example, a favorable change of at least 10% in a measurable parameter of disease, and preferably at least 20%, 30%, 40%, 50% or more can be indicative of effective treatment. Efficacy for a given iRNA drug or formulation of that drug can also be judged using an experimental animal model for the given disease as known in the art. When using an experimental animal model, efficacy of treatment is evidenced when a statistically significant reduction in a marker or symptom is observed.

Alternatively, the efficacy can be measured by a reduction in the severity of disease as determined by one skilled in the art of diagnosis based on a clinically accepted disease severity grading scale, as but one example the NYHA Classes of Heart failure. In this example, there are four stages of heart failure graded from mild to severe, based on symptoms such as e.g., the ability to carry on physical activity, shortness of breath, and palpitations. Efficacy can be measured in this example by the movement of a patient from e.g., a Class IV (severe) heart failure profile to a Class III, Class II, or Class I heart failure profile. Similar grading scales exist for many diseases and disorders, including, but not limited to heart disease, diabetic retinopathy, systemic sclerosis, *Clostridium difficile*-Associated Disease, Lipodystrophy (the Lipodystrophy Severity Grading Scale), HIV (the HIV Outpatient Study scale), cancer grading, cancer staging, etc., and can be used to determine a patient's progress in response to treatment. Any positive change resulting in e.g., lessening of severity of disease measured using the appropriate scale, represents adequate treatment using an iRNA or iRNA formulation as described herein.

Patients can be administered a therapeutic amount of iRNA, such as 0.01 mg/kg, 0.05 mg/kg, 0.1 mg/kg, 0.5 mg/kg, 1.0 mg/kg, 1.5 mg/kg, 2.0 mg/kg, or 2.5 mg/kg dsRNA. The iRNA can be administered by intravenous infusion over a period of time, such as over a 5 minute, 10 minute, 15 minute, 20 minute, or 25 minute period. The administration is repeated, for example, on a regular basis, such as biweekly (i.e., every two weeks) for one month, two months, three months, four months or longer. After an initial treatment regimen, the treatments can be administered on a less frequent basis. For example, after administration biweekly for three months, administration can be repeated once per month, for six months or a year or longer. Administration of the iRNA can reduce Mylip/Idol levels, e.g., in a cell, tissue, blood, urine or other compartment of the patient by at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80% or at least 90% or more.

Before administration of a full dose of the iRNA, patients can be administered a smaller dose, such as a 5% infusion reaction, and monitored for adverse effects, such as an allergic reaction, or for elevated lipid levels or blood pressure. In another example, the patient can be monitored for unwanted immunostimulatory effects, such as increased cytokine (e.g., TNF-alpha or INF-alpha) levels.

Many lipid diseases and disorders are hereditary. Therefore, a patient in need of a Mylip/Idol iRNA may be identified by taking a family history. A healthcare provider, such as a doctor, nurse, or family member, can take a family history before prescribing or administering a Mylip/Idol dsRNA. A DNA test may also be performed on the patient to identify a mutation in the Mylip/Idol gene, before a Mylip/Idol dsRNA is administered to the patient.

Owing to the inhibitory effects on Mylip/Idol expression, a composition according to the invention or a pharmaceutical composition prepared therefrom can enhance the quality of life.

Methods for Modulating Expression of a Mylip/Idol Gene

In yet another aspect, the invention provides a method for modulating (e.g., inhibiting or activating) the expression of a Mylip/Idol gene in a mammal.

In one embodiment, the method includes administering a composition featured in the invention to the mammal such that expression of the target Mylip/Idol gene is decreased, such as for an extended duration, e.g., at least two, three, four days or more, e.g., one week, two weeks, three weeks, or four weeks or longer. The effect of the decreased target Mylip/Idol gene preferably results in a decrease in LDLc levels in the blood, and more particularly in the serum, of the mammal. In some embodiments, LDLc levels are decreased by at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, or at least 60%, or more, as compared to pretreatment levels.

In another embodiment, the method includes administering a composition as described herein to a mammal such that expression of the target Mylip/Idol gene is increased by e.g., at least 10% compared to an untreated animal. In some embodiments, the activation of Mylip/Idol occurs over an extended duration, e.g., at least two, three, four days or more, e.g., one week, two weeks, three weeks, four weeks, or more. Without wishing to be bound by theory, an iRNA can activate Mylip/Idol expression by stabilizing the Mylip/Idol mRNA transcript, interacting with a promoter in the genome, and/or inhibiting an inhibitor of Mylip/Idol expression.

Preferably, the iRNAs useful for the methods and compositions featured in the invention specifically target RNAs (primary or processed) of the target Mylip/Idol gene. Compositions and methods for inhibiting the expression of these Mylip/Idol genes using iRNAs can be prepared and performed as described elsewhere herein.

In one embodiment, the method includes administering a composition containing an iRNA, where the iRNA includes a nucleotide sequence that is complementary to at least a part of an RNA transcript of the Mylip/Idol gene of the mammal to be treated. When the organism to be treated is a mammal such as a human, the composition may be administered by any means known in the art including, but not limited to oral, intraperitoneal, or parenteral routes, including intracranial (e.g., intraventricular, intraparenchymal and intrathecal), intravenous, intramuscular, subcutaneous, transdermal, airway (aerosol), nasal, rectal, and topical (including buccal and sublingual) administration. In certain embodiments, the compositions are administered by intravenous infusion or injection.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the iRNAs and methods featured in the invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

EXAMPLES

Example 1

Interference RNA (iRNA) Synthesis

Source of Reagents

Where the source of a reagent is not specifically given herein, such reagent may be obtained from any supplier of reagents for molecular biology at a quality/purity standard for application in molecular biology.

Oligonucleotide Synthesis.

Applicants have used several different methods to generate the iRNA molecules described herein. This Example describes one approach that has been used. The ordinarily skilled artisan can use any method known in the art to prepare iRNAs as described herein.

Oligonucleotides are synthesized on an AKTAoligopilot synthesizer. Commercially available controlled pore glass solid support (dT-CPG, 500Å, Prime Synthesis) and RNA phosphoramidites with standard protecting groups, 5'-O-dimethoxytrityl N6-benzoyl-2'-t-butyldimethylsilyl-adenosine-3'-O—N,N'-diisopropyl-2-cyanoethylphosphoramidite, 5'-O-dimethoxytrityl-N4-acetyl-2'-t-butyldimethylsilyl-cytidine-3'-O—N,N'-diisopropyl-2-cyanoethylphosphoramidite, 5'-O-dimethoxytrityl-N2-isobutryl-2'-t-butyldimethylsilyl-guanosine-3'-O—N,N'-diisopropyl-2-cyanoethylphosphoramidite, and 5'-O-dimethoxytrityl-2'-t-butyldimethylsilyl-uridine-3'-O—N,N'-diisopropyl-2-cyanoethylphosphoramidite (Pierce Nucleic Acids Technologies) were used for the oligonucleotide synthesis. The 2'-F phosphoramidites, 5'-O-dimethoxytrityl-N4-acetyl-2'-fluoro-cytidine-3'-O—N,N'-diisopropyl-2-cyanoethyl-phosphoramidite and 5'-O-dimethoxytrityl-2'-fluoro-uridine-3'-O—N,N'-diisopropyl-2-cyanoethyl-phosphoramidite are purchased from (Promega). All phosphoramidites are used at a concentration of 0.2M in acetonitrile (CH_3CN) except for guanosine which is used at 0.2M concentration in 10% THF/ANC (v/v). Coupling/recycling time of 16 minutes is used. The activator is 5-ethyl thiotetrazole (0.75M, American International Chemicals); for the PO-oxidation iodine/water/pyridine is used and for the PS-oxidation PADS (2%) in 2,6-lutidine/ACN (1:1 v/v) is used.

3'-ligand conjugated strands are synthesized using solid support containing the corresponding ligand. For example, the introduction of cholesterol unit in the sequence is performed from a hydroxyprolinol-cholesterol phosphoramidite. Cholesterol is tethered to trans-4-hydroxyprolinol via a 6-aminohexanoate linkage to obtain a hydroxyprolinol-cholesterol moiety. 5'-end Cy-3 and Cy-5.5 (fluorophore) labeled iRNAs are synthesized from the corresponding Quasar-570 (Cy-3) phosphoramidite are purchased from Biosearch Technologies. Conjugation of ligands to 5'-end and or internal position is achieved by using appropriately protected ligand-phosphoramidite building block. An extended 15 min coupling of 0.1 M solution of phosphoramidite in anhydrous CH_3CN in the presence of 5-(ethylthio)-1H-tetrazole activator to a solid-support-bound oligonucleotide. Oxidation of the internucleotide phosphite to the phosphate is carried out using standard iodine-water as reported (1) or by treatment with tert-butyl hydroperoxide/acetonitrile/water (10:87:3) with 10 min oxidation wait time conjugated oligonucleotide. Phosphorothioate is introduced by the oxidation of phosphite to phosphorothioate by using a sulfur transfer reagent such as DDTT (purchased from AM Chemicals), PADS and or Beaucage reagent. The cholesterol phosphoramidite is synthesized in house and used at a concentration of 0.1 M in dichloromethane. Coupling time for the cholesterol phosphoramidite is 16 minutes.

Deprotection I (Nucleobase Deprotection)

After completion of synthesis, the support is transferred to a 100 mL glass bottle (VWR). The oligonucleotide is cleaved from the support with simultaneous deprotection of base and phosphate groups with 80 mL of a mixture of ethanolic ammonia [ammonia:ethanol (3:1)] for 6.5 h at 55° C. The bottle is cooled briefly on ice and then the ethanolic ammonia mixture is filtered into a new 250-mL bottle. The CPG is washed with 2×40 mL portions of ethanol/water (1:1 v/v). The volume of the mixture is then reduced to ~30 mL by roto-vap. The mixture is then frozen on dry ice and dried under vacuum on a speed vac.

Deprotection II (Removal of 2'-TBDMS Group)

The dried residue is resuspended in 26 mL of triethylamine, triethylamine trihydrofluoride (TEA.3HF) or pyridine-HF and DMSO (3:4:6) and heated at 60° C. for 90 minutes to remove the tert-butyldimethylsilyl (TBDMS) groups at the 2' position. The reaction is then quenched with 50 mL of 20 mM sodium acetate and the pH is adjusted to 6.5. Oligonucleotide is stored in a freezer until purification.

Analysis

The oligonucleotides are analyzed by high-performance liquid chromatography (HPLC) prior to purification and selection of buffer and column depends on nature of the sequence and or conjugated ligand.

HPLC Purification

The ligand-conjugated oligonucleotides are purified by reverse-phase preparative HPLC. The unconjugated oligonucleotides are purified by anion-exchange HPLC on a TSK gel column packed in house. The buffers are 20 mM sodium phosphate (pH 8.5) in 10% CH_3CN (buffer A) and 20 mM sodium phosphate (pH 8.5) in 10% CH_3CN, 1M NaBr (buffer B). Fractions containing full-length oligonucleotides are pooled, desalted, and lyophilized. Approximately 0.15 OD of desalted oligonucleotides are diluted in water to 150 μL and then pipetted into special vials for CGE and LC/MS analysis. Compounds are then analyzed by LC-ESMS and CGE.

iRNA Preparation

For the general preparation of iRNA, equimolar amounts of sense and antisense strand are heated in 1×PBS at 95° C. for 5 min and slowly cooled to room temperature. Integrity of the duplex is confirmed by HPLC analysis.

Nucleic acid sequences are represented below using standard nomenclature, and specifically the abbreviations of Table 2.

TABLE 2

Abbreviations of nucleotide monomers used in nucleic acid sequence representation. It will be understood that these monomers, when present in an oligonucleotide, are mutually linked by 5'-3'-phosphodiester bonds.

Abbreviation	Nucleotide(s)
A	adenosine
C	cytidine
G	guanosine
T	thymidine
U	uridine
N	any nucleotide (G, A, C, T or U)
a	2'-O-methyladenosine
c	2'-O-methylcytidine
g	2'-O-methylguanosine
u	2'-O-methyruridine

TABLE 2-continued

Abbreviations of nucleotide monomers used in nucleic acid sequence representation. It will be understood that these monomers, when present in an oligonucleotide, are mutually linked by 5'-3'-phosphodiester bonds.

Abbreviation	Nucleotide(s)
dT	2'-deoxythymidine
s	phosphorothioate linkage

Example 2

Mylip/Idol siRNA Design

Transcripts

siRNAs targeting Mylip/Idol were designed and synthesized. The design used human transcript NM_013262.3 (SEQ ID NO: 644, FIG. **1**) and rat transcript NM_153789.3 (SEQ ID NO: 642) from the NCBI Refseq collection.

siRNA duplexes were designed with 100% identity to the Mylip/Idol gene.

A total of 151 sense and 151 antisense human Mylip/Idol derived siRNA oligos were synthesized and formed into duplexes. The oligos are presented in Tables 3 and 5 (human Mylip/Idol). In addition, 33 sense and 33 antisense rat Mylip/Idol derived siRNA oligos were synthesized and formed into duplexes (see e.g., Tables 4 and 6).

TABLE 3

Sense and antisense strand sequences of human Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_013262.3, SEQ ID NO: 644)	Sequence (5' to 3')	SEQ ID NO:	Sequence with 3' dinucleotide overhang (5' to 3')	SEQ ID NO:
S	240	GCUGUGUUAUGUGACGAGG	20	GCUGUGUUAUGUGACGAGGNN	94
AS	240	CCUCGUCACAUAACACAGC	21	CCUCGUCACAUAACACAGCNN	95
S	241	CUGUGUUAUGUGACGAGGC	22	CUGUGUUAUGUGACGAGGCNN	96
AS	241	GCCUCGUCACAUAACACAG	23	GCCUCGUCACAUAACACAGNN	97
S	244	UGUUAUGUGACGAGGCCGG	24	UGUUAUGUGACGAGGCCGGNN	98
AS	244	CCGGCCUCGUCACAUAACA	25	CCGGCCUCGUCACAUAACANN	99
S	245	GUUAUGUGACGAGGCCGGA	26	GUUAUGUGACGAGGCCGGANN	100
AS	245	UCCGGCCUCGUCACAUAAC	27	UCCGGCCUCGUCACAUAACNN	101
S	246	UUAUGUGACGAGGCCGGAC	28	UUAUGUGACGAGGCCGGACNN	102
AS	246	GUCCGGCCUCGUCACAUAA	29	GUCCGGCCUCGUCACAUAANN	103
S	247	UAUGUGACGAGGCCGGACG	30	UAUGUGACGAGGCCGGACGNN	104
AS	247	CGUCCGGCCUCGUCACAUA	31	CGUCCGGCCUCGUCACAUANN	105
S	248	AUGUGACGAGGCCGGACGC	32	AUGUGACGAGGCCGGACGCNN	106
AS	248	GCGUCCGGCCUCGUCACAU	33	GCGUCCGGCCUCGUCACAUNN	107
S	249	UGUGACGAGGCCGGACGCG	34	UGUGACGAGGCCGGACGCGNN	108
AS	249	CGCGUCCGGCCUCGUCACA	35	CGCGUCCGGCCUCGUCACANN	109
S	290	AGGCGAAAGCCAACGGCGA	36	AGGCGAAAGCCAACGGCGANN	110
AS	290	UCGCCGUUGGCUUUCGCCU	37	UCGCCGUUGGCUUUCGCCUNN	111

TABLE 3-continued

Sense and antisense strand sequences of human Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_013262.3, SEQ ID NO: 644)	Sequence (5' to 3')	SEQ ID NO:	Sequence with 3' dinucleotide overhang (5' to 3')	SEQ ID NO:
S	291	GGCGAAAGCCAACGGCGAG	38	GGCGAAAGCCAACGGCGAGNN	112
AS	291	CUCGCCGUUGGCUUUCGCC	39	CUCGCCGUUGGCUUUCGCCNN	113
S	331	AGGCGACUGGGAAUCAUAG	40	AGGCGACUGGGAAUCAUAGNN	114
AS	331	CUAUGAUUCCCAGUCGCCU	41	CUAUGAUUCCCAGUCGCCUNN	115
S	332	GGCGACUGGGAAUCAUAGA	42	GGCGACUGGGAAUCAUAGANN	116
AS	332	UCUAUGAUUCCCAGUCGCC	43	UCUAUGAUUCCCAGUCGCCNN	117
S	333	GCGACUGGGAAUCAUAGAA	44	GCGACUGGGAAUCAUAGAANN	118
AS	333	UUCUAUGAUUCCCAGUCGC	45	UUCUAUGAUUCCCAGUCGCNN	119
S	368	UGCAGUUUACGGGUAGCAA	46	UGCAGUUUACGGGUAGCAANN	120
AS	368	UUGCUACCCGUAAACUGCA	47	UUGCUACCCGUAAACUGCANN	121
S	369	GCAGUUUACGGGUAGCAAA	48	GCAGUUUACGGGUAGCAAANN	122
AS	369	UUUGCUACCCGUAAACUGC	49	UUUGCUACCCGUAAACUGCNN	123
S	370	CAGUUUACGGGUAGCAAAG	50	CAGUUUACGGGUAGCAAAGNN	124
AS	370	CUUUGCUACCCGUAAACUG	51	CUUUGCUACCCGUAAACUGNN	125
S	371	AGUUUACGGGUAGCAAAGG	52	AGUUUACGGGUAGCAAAGGNN	126
AS	371	CCUUUGCUACCCGUAAACU	53	CCUUUGCUACCCGUAAACUNN	127
S	372	GUUUACGGGUAGCAAAGGU	54	GUUUACGGGUAGCAAAGGUNN	128
AS	372	ACCUUUGCUACCCGUAAAC	55	ACCUUUGCUACCCGUAAACNN	129
S	373	UUUACGGGUAGCAAAGGUG	56	UUUACGGGUAGCAAAGGUGNN	130
AS	373	CACCUUUGCUACCCGUAAA	57	CACCUUUGCUACCCGUAAANN	131
S	386	AAGGUGAAAGUUUAUGGCU	58	AAGGUGAAAGUUUAUGGCUNN	132
AS	386	AGCCAUAAACUUUCACCUU	59	AGCCAUAAACUUUCACCUUNN	133
S	387	AGGUGAAAGUUUAUGGCUA	60	AGGUGAAAGUUUAUGGCUANN	134
AS	387	UAGCCAUAAACUUUCACCU	61	UAGCCAUAAACUUUCACCUNN	135
S	388	GGUGAAAGUUUAUGGCUAA	62	GGUGAAAGUUUAUGGCUAANN	136
AS	388	UUAGCCAUAAACUUUCACC	63	UUAGCCAUAAACUUUCACCNN	137
S	393	AAGUUUAUGGCUAAACCUG	64	AAGUUUAUGGCUAAACCUGNN	138
AS	393	CAGGUUUAGCCAUAAACUU	65	CAGGUUUAGCCAUAAACUUNN	139
S	395	GUUUAUGGCUAAACCUGAG	66	GUUUAUGGCUAAACCUGAGNN	140
AS	395	CUCAGGUUUAGCCAUAAAC	67	CUCAGGUUUAGCCAUAAACNN	141
S	434	UGGAUGGGCUAGCCCCUUA	68	UGGAUGGGCUAGCCCCUUANN	142
AS	434	UAAGGGGCUAGCCCAUCCA	69	UAAGGGGCUAGCCCAUCCANN	143
S	435	GGAUGGGCUAGCCCCUUAC	70	GGAUGGGCUAGCCCCUUACNN	144
AS	435	GUAAGGGGCUAGCCCAUCC	71	GUAAGGGGCUAGCCCAUCCNN	145
S	438	UGGGCUAGCCCCUUACAGG	72	UGGGCUAGCCCCUUACAGGNN	146
AS	438	CCUGUAAGGGGCUAGCCCA	73	CCUGUAAGGGGCUAGCCCANN	147

TABLE 3-continued

Sense and antisense strand sequences of human Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_013262.3, SEQ ID NO: 644)	Sequence (5' to 3')	SEQ ID NO:	Sequence with 3' dinucleotide overhang (5' to 3')	SEQ ID NO:
S	439	GGGCUAGCCCCUUACAGGC	74	GGGCUAGCCCCUUACAGGCNN	148
AS	439	GCCUGUAAGGGGCUAGCCC	75	GCCUGUAAGGGGCUAGCCCNN	149
S	440	GGCUAGCCCCUUACAGGCU	76	GGCUAGCCCCUUACAGGCUNN	150
AS	440	AGCCUGUAAGGGGCUAGCC	77	AGCCUGUAAGGGGCUAGCCNN	151
S	444	AGCCCCUUACAGGCUUAAA	78	AGCCCCUUACAGGCUUAAANN	152
AS	444	UUUAAGCCUGUAAGGGGCU	79	UUUAAGCCUGUAAGGGGCUNN	153
S	446	CCCCUUACAGGCUUAAACU	80	CCCCUUACAGGCUUAAACUNN	154
AS	446	AGUUUAAGCCUGUAAGGGG	81	AGUUUAAGCCUGUAAGGGGNN	155
S	498	CUUACAGGAGCAGACUAGG	82	CUUACAGGAGCAGACUAGGNN	156
AS	498	CCUAGUCUGCUCCUGUAAG	83	CCUAGUCUGCUCCUGUAAGNN	157
S	508	CAGACUAGGCAUAUCUUUU	84	CAGACUAGGCAUAUCUUUUNN	158
AS	508	AAAAGAUAUGCCUAGUCUG	85	AAAAGAUAUGCCUAGUCUGNN	159
S	640	ACUGCCAAGUAUAACUAUG	86	ACUGCCAAGUAUAACUAUGNN	160
AS	640	CAUAGUUAUACUUGGCAGU	87	CAUAGUUAUACUUGGCAGUNN	161
S	763	UUGCAGAUUGUGUCGGCAA	88	UUGCAGAUUGUGUCGGCAANN	162
AS	763	UUGCCGACACAAUCUGCAA	89	UUGCCGACACAAUCUGCAANN	163
S	764	UGCAGAUUGUGUCGGCAAU	90	UGCAGAUUGUGUCGGCAAUNN	164
AS	764	AUUGCCGACACAAUCUGCA	91	AUUGCCGACACAAUCUGCANN	165
S	765	GCAGAUUGUGUCGGCAAUG	92	GCAGAUUGUGUCGGCAAUGNN	166
AS	765	CAUUGCCGACACAAUCUGC	93	CAUUGCCGACACAAUCUGCNN	167
S	233	CAGCCAUGCUGUGUUAUGU	648	CAGCCAUGCUGUGUUAUGUNN	876
AS	233	ACAUAACACAGCAUGGCUG	649	ACAUAACACAGCAUGGCUGNN	877
S	330	CAGGCGACUGGGAAUCAUA	650	CAGGCGACUGGGAAUCAUANN	878
AS	330	UAUGAUUCCCAGUCGCCUG	651	UAUGAUUCCCAGUCGCCUGNN	879
S	335	GACUGGGAAUCAUAGAAGU	652	GACUGGGAAUCAUAGAAGUNN	880
AS	335	ACUUCUAUGAUUCCCAGUC	653	ACUUCUAUGAUUCCCAGUCNN	881
S	336	ACUGGGAAUCAUAGAAGUU	654	ACUGGGAAUCAUAGAAGUUNN	882
AS	336	AACUUCUAUGAUUCCCAGU	655	AACUUCUAUGAUUCCCAGUNN	883
S	341	GAAUCAUAGAAGUUGACUA	656	GAAUCAUAGAAGUUGACUANN	884
AS	341	UAGUCAACUUCUAUGAUUC	657	UAGUCAACUUCUAUGAUUCNN	885
S	404	UAAACCUGAGAAACCGGAU	658	UAAACCUGAGAAACCGGAUNN	886
AS	404	AUCCGGUUUCUCAGGUUUA	659	AUCCGGUUUCUCAGGUUUANN	887
S	454	AGGCUUAAACUUAGAGUCA	660	AGGCUUAAACUUAGAGUCANN	888
AS	454	UGACUCUAAGUUUAAGCCU	661	UGACUCUAAGUUUAAGCCUNN	889
S	455	GGCUUAAACUUAGAGUCAA	662	GGCUUAAACUUAGAGUCAANN	890

TABLE 3-continued

Sense and antisense strand sequences of human Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_013262.3, SEQ ID NO: 644)	Sequence (5' to 3')	SEQ ID NO:	Sequence with 3' dinucleotide overhang (5' to 3')	SEQ ID NO:
AS	455	UUGACUCUAAGUUUAAGCC	663	UUGACUCUAAGUUUAAGCCNN	891
S	501	ACAGGAGCAGACUAGGCAU	664	ACAGGAGCAGACUAGGCAUNN	892
AS	501	AUGCCUAGUCUGCUCCUGU	665	AUGCCUAGUCUGCUCCUGUNN	893
S	502	CAGGAGCAGACUAGGCAUA	666	CAGGAGCAGACUAGGCAUANN	894
AS	502	UAUGCCUAGUCUGCUCCUG	667	UAUGCCUAGUCUGCUCCUGNN	895
S	505	GAGCAGACUAGGCAUAUCU	668	GAGCAGACUAGGCAUAUCUNN	896
AS	505	AGAUAUGCCUAGUCUGCUC	669	AGAUAUGCCUAGUCUGCUCNN	897
S	507	GCAGACUAGGCAUAUCUUU	670	GCAGACUAGGCAUAUCUUUNN	898
AS	507	AAAGAUAUGCCUAGUCUGC	671	AAAGAUAUGCCUAGUCUGCNN	899
S	550	UUGGCAGGCCACCUCUUGU	672	UUGGCAGGCCACCUCUUGUNN	900
AS	550	ACAAGAGGUGGCCUGCCAA	673	ACAAGAGGUGGCCUGCCAANN	901
S	694	UUGAACAGCAUUGUUGCAA	674	UUGAACAGCAUUGUUGCAANN	902
AS	694	UUGCAACAAUGCUGUUCAA	675	UUGCAACAAUGCUGUUCAANN	903
S	746	CAGCUGAAUACCAAGUUUU	676	CAGCUGAAUACCAAGUUUUNN	904
AS	746	AAAACUUGGUAUUCAGCUG	677	AAAACUUGGUAUUCAGCUGNN	905
S	774	GUCGGCAAUGGAAAACUAU	678	GUCGGCAAUGGAAAACUAUNN	906
AS	774	AUAGUUUUCCAUUGCCGAC	679	AUAGUUUUCCAUUGCCGACNN	907
S	788	ACUAUGGCAUAGAAUGGCA	680	ACUAUGGCAUAGAAUGGCANN	908
AS	788	UGCCAUUCUAUGCCAUAGU	681	UGCCAUUCUAUGCCAUAGUNN	909
S	807	UUCUGUGCGGGAUAGCGAA	682	UUCUGUGCGGGAUAGCGAANN	910
AS	807	UUCGCUAUCCCGCACAGAA	683	UUCGCUAUCCCGCACAGAANN	911
S	850	GGACCUGAAGGAAUCUCAA	684	GGACCUGAAGGAAUCUCAANN	912
AS	850	UUGAGAUUCCUUCAGGUCC	685	UUGAGAUUCCUUCAGGUCCNN	913
S	873	UAAAGAUGACUUUAGCCCA	686	UAAAGAUGACUUUAGCCCANN	914
AS	873	UGGGCUAAAGUCAUCUUUA	687	UGGGCUAAAGUCAUCUUUANN	915
S	874	AAAGAUGACUUUAGCCCAA	688	AAAGAUGACUUUAGCCCAANN	916
AS	874	UUGGGCUAAAGUCAUCUUU	689	UUGGGCUAAAGUCAUCUUUNN	917
S	885	UAGCCCAAUUAAUAGGAUA	690	UAGCCCAAUUAAUAGGAUANN	918
AS	885	UAUCCUAUUAAUUGGGCUA	691	UAUCCUAUUAAUUGGGCUANN	919
S	889	CCAAUUAAUAGGAUAGCUU	692	CCAAUUAAUAGGAUAGCUUNN	920
AS	889	AAGCUAUCCUAUUAAUUGG	693	AAGCUAUCCUAUUAAUUGGNN	921
S	894	UAAUAGGAUAGCUUAUCCU	694	UAAUAGGAUAGCUUAUCCUNN	922
AS	894	AGGAUAAGCUAUCCUAUUA	695	AGGAUAAGCUAUCCUAUUANN	923
S	978	CAGCAUCGUGCUCUUGUUU	696	CAGCAUCGUGCUCUUGUUUNN	924
AS	978	AAACAAGAGCACGAUGCUG	697	AAACAAGAGCACGAUGCUGNN	925
S	981	CAUCGUGCUCUUGUUUAAA	698	CAUCGUGCUCUUGUUUAAANN	926

TABLE 3-continued

Sense and antisense strand sequences of human Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_013262.3, SEQ ID NO: 644)	Sequence (5' to 3')	SEQ ID NO:	Sequence with 3' dinucleotide overhang (5' to 3')	SEQ ID NO:
AS	981	UUUAAACAAGAGCACGAUG	699	UUUAAACAAGAGCACGAUGNN	927
S	1024	GGGCUCUACCGAGCGAUAA	700	GGGCUCUACCGAGCGAUAANN	928
AS	1024	UUAUCGCUCGGUAGAGCCC	701	UUAUCGCUCGGUAGAGCCCNN	929
S	1026	GCUCUACCGAGCGAUAACA	702	GCUCUACCGAGCGAUAACANN	930
AS	1026	UGUUAUCGCUCGGUAGAGC	703	UGUUAUCGCUCGGUAGAGCNN	931
S	1028	UCUACCGAGCGAUAACAGA	704	UCUACCGAGCGAUAACAGANN	932
AS	1028	UCUGUUAUCGCUCGGUAGA	705	UCUGUUAUCGCUCGGUAGANN	933
S	1030	UACCGAGCGAUAACAGAGA	706	UACCGAGCGAUAACAGAGANN	934
AS	1030	UCUCUGUUAUCGCUCGGUA	707	UCUCUGUUAUCGCUCGGUANN	935
S	1042	ACAGAGACGCACGCAUUCU	708	ACAGAGACGCACGCAUUCUNN	936
AS	1042	AGAAUGCGUGCGUCUCUGU	709	AGAAUGCGUGCGUCUCUGUNN	937
S	1113	GAAGGGCCACUUGGCAUCU	710	GAAGGGCCACUUGGCAUCUNN	938
AS	1113	AGAUGCCAAGUGGCCCUUC	711	AGAUGCCAAGUGGCCCUUCNN	939
S	1190	CAUCAAAGGAGGUGUAUGA	712	CAUCAAAGGAGGUGUAUGANN	940
AS	1190	UCAUACACCUCCUUUGAUG	713	UCAUACACCUCCUUUGAUGNN	941
S	1237	GGCGUUGUGGACCUCGUUU	714	GGCGUUGUGGACCUCGUUUNN	942
AS	1237	AAACGAGGUCCACAACGCC	715	AAACGAGGUCCACAACGCCNN	943
S	1240	GUUGUGGACCUCGUUUCAA	716	GUUGUGGACCUCGUUUCAANN	944
AS	1240	UUGAAACGAGGUCCACAAC	717	UUGAAACGAGGUCCACAACNN	945
S	1242	UGUGGACCUCGUUUCAAGA	718	UGUGGACCUCGUUUCAAGANN	946
AS	1242	UCUUGAAACGAGGUCCACA	719	UCUUGAAACGAGGUCCACANN	947
S	1279	CACUCGCCUCUGAAGUCCU	720	CACUCGCCUCUGAAGUCCUNN	948
AS	1279	AGGACUUCAGAGGCGAGUG	721	AGGACUUCAGAGGCGAGUGNN	949
S	1515	GCAUGUCCAGCACGUCUAU	722	GCAUGUCCAGCACGUCUAUNN	950
AS	1515	AUAGACGUGCUGGACAUGC	723	AUAGACGUGCUGGACAUGCNN	951
S	1517	AUGUCCAGCACGUCUAUCU	724	AUGUCCAGCACGUCUAUCUNN	952
AS	1517	AGAUAGACGUGCUGGACAU	725	AGAUAGACGUGCUGGACAUNN	953
S	1555	CUCAAUCUGACUGUAAUCU	726	CUCAAUCUGACUGUAAUCUNN	954
AS	1555	AGAUUACAGUCAGAUUGAG	727	AGAUUACAGUCAGAUUGAGNN	955
S	1557	CAAUCUGACUGUAAUCUAA	728	CAAUCUGACUGUAAUCUAANN	956
AS	1557	UUAGAUUACAGUCAGAUUG	729	UUAGAUUACAGUCAGAUUGNN	957
S	1558	AAUCUGACUGUAAUCUAAU	730	AAUCUGACUGUAAUCUAAUNN	958
AS	1558	AUUAGAUUACAGUCAGAUU	731	AUUAGAUUACAGUCAGAUUNN	959
S	1616	UGCACUAUUAUAAACUAUU	732	UGCACUAUUAUAAACUAUUNN	960
AS	1616	AAUAGUUUAUAAUAGUGCA	733	AAUAGUUUAUAAUAGUGCANN	961

TABLE 3-continued

Sense and antisense strand sequences of human Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_013262.3, SEQ ID NO: 644)	Sequence (5' to 3')	SEQ ID NO:	Sequence with 3' dinucleotide overhang (5' to 3')	SEQ ID NO:
S	1715	AUAACACAGCUACUCCUCA	734	AUAACACAGCUACUCCUCANN	962
AS	1715	UGAGGAGUAGCUGUGUUAU	735	UGAGGAGUAGCUGUGUUAUNN	963
S	1740	AAACAUAUCCAUGCGUAGA	736	AAACAUAUCCAUGCGUAGANN	964
AS	1740	UCUACGCAUGGAUAUGUUU	737	UCUACGCAUGGAUAUGUUUNN	965
S	1741	AACAUAUCCAUGCGUAGAA	738	AACAUAUCCAUGCGUAGAANN	966
AS	1741	UUCUACGCAUGGAUAUGUU	739	UUCUACGCAUGGAUAUGUUNN	967
S	1744	AUAUCCAUGCGUAGAAUCA	740	AUAUCCAUGCGUAGAAUCANN	968
AS	1744	UGAUUCUACGCAUGGAUAU	741	UGAUUCUACGCAUGGAUAUNN	969
S	1745	UAUCCAUGCGUAGAAUCAA	742	UAUCCAUGCGUAGAAUCAANN	970
AS	1745	UUGAUUCUACGCAUGGAUA	743	UUGAUUCUACGCAUGGAUANN	971
S	1753	CGUAGAAUCAACAACUCCA	744	CGUAGAAUCAACAACUCCANN	972
AS	1753	UGGAGUUGUUGAUUCUACG	745	UGGAGUUGUUGAUUCUACGNN	973
S	1837	CUAGUAAAGGAAUAGGUAA	746	CUAGUAAAGGAAUAGGUAANN	974
AS	1837	UUACCUAUUCCUUUACUAG	747	UUACCUAUUCCUUUACUAGNN	975
S	1838	UAGUAAAGGAAUAGGUAAA	748	UAGUAAAGGAAUAGGUAAANN	976
AS	1838	UUUACCUAUUCCUUUACUA	749	UUUACCUAUUCCUUUACUANN	977
S	1842	AAAGGAAUAGGUAAAGUCU	750	AAAGGAAUAGGUAAAGUCUNN	978
AS	1842	AGACUUUACCUAUUCCUUU	751	AGACUUUACCUAUUCCUUUNN	979
S	1843	AAGGAAUAGGUAAAGUCUU	752	AAGGAAUAGGUAAAGUCUUNN	980
AS	1843	AAGACUUUACCUAUUCCUU	753	AAGACUUUACCUAUUCCUUNN	981
S	1871	UGAAGUGGCAACAUAGCCA	754	UGAAGUGGCAACAUAGCCANN	982
AS	1871	UGGCUAUGUUGCCACUUCA	755	UGGCUAUGUUGCCACUUCANN	983
S	1872	GAAGUGGCAACAUAGCCAA	756	GAAGUGGCAACAUAGCCAANN	984
AS	1872	UUGGCUAUGUUGCCACUUC	757	UUGGCUAUGUUGCCACUUCNN	985
S	1893	AGUUGGGUACCUUUUAGGA	758	AGUUGGGUACCUUUUAGGANN	986
AS	1893	UCCUAAAAGGUACCCAACU	759	UCCUAAAAGGUACCCAACUNN	987
S	1915	GAUGUUGUAAGUCUCCUUA	760	GAUGUUGUAAGUCUCCUUANN	988
AS	1915	UAAGGAGACUUACAACAUC	761	UAAGGAGACUUACAACAUCNN	989
S	1921	GUAAGUCUCCUUAAUGUAU	762	GUAAGUCUCCUUAAUGUAUNN	990
AS	1921	AUACAUUAAGGAGACUUAC	763	AUACAUUAAGGAGACUUACNN	991
S	1933	AAUGUAUCCUGAGGUAAGU	764	AAUGUAUCCUGAGGUAAGUNN	992
AS	1933	ACUUACCUCAGGAUACAUU	765	ACUUACCUCAGGAUACAUUNN	993
S	1939	UCCUGAGGUAAGUUUCCUA	766	UCCUGAGGUAAGUUUCCUANN	994
AS	1939	UAGGAAACUUACCUCAGGA	767	UAGGAAACUUACCUCAGGANN	995
S	1954	CCUACUGGCAGCAGAUUUU	768	CCUACUGGCAGCAGAUUUUNN	996
AS	1954	AAAAUCUGCUGCCAGUAGG	769	AAAAUCUGCUGCCAGUAGGNN	997

TABLE 3-continued

Sense and antisense strand sequences of human Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_013262.3, SEQ ID NO: 644)	Sequence (5' to 3')	SEQ ID NO:	Sequence with 3' dinucleotide overhang (5' to 3')	SEQ ID NO:
S	2046	UUUUGUAAAUUGUUGUCGU	770	UUUUGUAAAUUGUUGUCGUNN	998
AS	2046	ACGACAACAAUUUACAAAA	771	ACGACAACAAUUUACAAAANN	999
S	2049	UGUAAAUUGUUGUCGUUUU	772	UGUAAAUUGUUGUCGUUUUNN	1000
AS	2049	AAAACGACAACAAUUUACA	773	AAAACGACAACAAUUUACANN	1001
S	2103	GAUUGGAAGGCAAACAGGU	774	GAUUGGAAGGCAAACAGGUNN	1002
AS	2103	ACCUGUUUGCCUUCCAAUC	775	ACCUGUUUGCCUUCCAAUCNN	1003
S	2109	AAGGCAAACAGGUUUACAA	776	AAGGCAAACAGGUUUACAANN	1004
AS	2109	UUGUAAACCUGUUUGCCUU	777	UUGUAAACCUGUUUGCCUUNN	1005
S	2159	UGUUGUCAGAUUUAAACCA	778	UGUUGUCAGAUUUAAACCANN	1006
AS	2159	UGGUUUAAAUCUGACAACA	779	UGGUUUAAAUCUGACAACANN	1007
S	2172	AAACCAGUGUGGCUAGUAA	780	AAACCAGUGUGGCUAGUAANN	1008
AS	2172	UUACUAGCCACACUGGUUU	781	UUACUAGCCACACUGGUUUNN	1009
S	2206	AUGUGGGUGGCUCCCUAUU	782	AUGUGGGUGGCUCCCUAUUNN	1010
AS	2206	AAUAGGGAGCCACCCACAU	783	AAUAGGGAGCCACCCACAUNN	1011
S	2248	CCCCACAAGCCUUUCGAUU	784	CCCCACAAGCCUUUCGAUUNN	1012
AS	2248	AAUCGAAAGGCUUGUGGGG	785	AAUCGAAAGGCUUGUGGGGNN	1013
S	2256	GCCUUUCGAUUAUAAAAUA	786	GCCUUUCGAUUAUAAAAUANN	1014
AS	2256	UAUUUUAUAAUCGAAAGGC	787	UAUUUUAUAAUCGAAAGGCNN	1015
S	2262	CGAUUAUAAAAUACUACCA	788	CGAUUAUAAAAUACUACCANN	1016
AS	2262	UGGUAGUAUUUUAUAAUCG	789	UGGUAGUAUUUUAUAAUCGNN	1017
S	2283	CUUGUUAUAAGAUUACUGU	790	CUUGUUAUAAGAUUACUGUNN	1018
AS	2283	ACAGUAAUCUUAUAACAAG	791	ACAGUAAUCUUAUAACAAGNN	1019
S	2293	GAUUACUGUGGAGUAGUCA	792	GAUUACUGUGGAGUAGUCANN	1020
AS	2293	UGACUACUCCACAGUAAUC	793	UGACUACUCCACAGUAAUCNN	1021
S	2296	UACUGUGGAGUAGUCAAGU	794	UACUGUGGAGUAGUCAAGUNN	1022
AS	2296	ACUUGACUACUCCACAGUA	795	ACUUGACUACUCCACAGUANN	1023
S	2428	GUACAACUGAGGGUAGUUA	796	GUACAACUGAGGGUAGUUANN	1024
AS	2428	UAACUACCCUCAGUUGUAC	797	UAACUACCCUCAGUUGUACNN	1025
S	2429	UACAACUGAGGGUAGUUAA	798	UACAACUGAGGGUAGUUAANN	1026
AS	2429	UUAACUACCCUCAGUUGUA	799	UUAACUACCCUCAGUUGUANN	1027
S	2431	CAACUGAGGGUAGUUAACU	800	CAACUGAGGGUAGUUAACUNN	1028
AS	2431	AGUUAACUACCCUCAGUUG	801	AGUUAACUACCCUCAGUUGNN	1029
S	2433	ACUGAGGGUAGUUAACUCA	802	ACUGAGGGUAGUUAACUCANN	1030
AS	2433	UGAGUUAACUACCCUCAGU	803	UGAGUUAACUACCCUCAGUNN	1031
S	2434	CUGAGGGUAGUUAACUCAU	804	CUGAGGGUAGUUAACUCAUNN	1032

TABLE 3-continued

Sense and antisense strand sequences of human Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_013262.3, SEQ ID NO: 644)	Sequence (5' to 3')	SEQ ID NO:	Sequence with 3' dinucleotide overhang (5' to 3')	SEQ ID NO:
AS	2434	AUGAGUUAACUACCCUCAG	805	AUGAGUUAACUACCCUCAGNN	1033
S	2436	GAGGGUAGUUAACUCAUCA	806	GAGGGUAGUUAACUCAUCANN	1034
AS	2436	UGAUGAGUUAACUACCCUC	807	UGAUGAGUUAACUACCCUCNN	1035
S	2438	GGGUAGUUAACUCAUCACU	808	GGGUAGUUAACUCAUCACUNN	1036
AS	2438	AGUGAUGAGUUAACUACCC	809	AGUGAUGAGUUAACUACCCNN	1037
S	2439	GGUAGUUAACUCAUCACUU	810	GGUAGUUAACUCAUCACUUNN	1038
AS	2439	AAGUGAUGAGUUAACUACC	811	AAGUGAUGAGUUAACUACCNN	1039
S	2441	UAGUUAACUCAUCACUUCU	812	UAGUUAACUCAUCACUUCUNN	1040
AS	2441	AGAAGUGAUGAGUUAACUA	813	AGAAGUGAUGAGUUAACUANN	1041
S	2489	UGGUGUUGCUUUGCUUGAA	814	UGGUGUUGCUUUGCUUGAANN	1042
AS	2489	UUCAAGCAAAGCAACACCA	815	UUCAAGCAAAGCAACACCANN	1043
S	2523	AUAGCCUUACCAUAAGUAU	816	AUAGCCUUACCAUAAGUAUNN	1044
AS	2523	AUACUUAUGGUAAGGCUAU	817	AUACUUAUGGUAAGGCUAUNN	1045
S	2530	UACCAUAAGUAUUUAGAUA	818	UACCAUAAGUAUUUAGAUANN	1046
AS	2530	UAUCUAAAUACUUAUGGUA	819	UAUCUAAAUACUUAUGGUANN	1047
S	2597	AAGUAAGUGCUUAAGUAUU	820	AAGUAAGUGCUUAAGUAUUNN	1048
AS	2597	AAUACUUAAGCACUUACUU	821	AAUACUUAAGCACUUACUUNN	1049
S	2610	AGUAUUAACUUUGGGUUGU	822	AGUAUUAACUUUGGGUUGUNN	1050
AS	2610	ACAACCCAAAGUUAAUACU	823	ACAACCCAAAGUUAAUACUNN	1051
S	2636	GUAUGUUUCGAAGGGGUUU	824	GUAUGUUUCGAAGGGGUUUNN	1052
AS	2636	AAACCCCUUCGAAACAUAC	825	AAACCCCUUCGAAACAUACNN	1053
S	2717	CUGGUCAGCUAGCAGGUUU	826	CUGGUCAGCUAGCAGGUUUNN	1054
AS	2717	AAACCUGCUAGCUGACCAG	827	AAACCUGCUAGCUGACCAGNN	1055
S	2718	UGGUCAGCUAGCAGGUUUU	828	UGGUCAGCUAGCAGGUUUUNN	1056
AS	2718	AAAACCUGCUAGCUGACCA	829	AAAACCUGCUAGCUGACCANN	1057
S	2720	GUCAGCUAGCAGGUUUUCU	830	GUCAGCUAGCAGGUUUUCUNN	1058
AS	2720	AGAAAACCUGCUAGCUGAC	831	AGAAAACCUGCUAGCUGACNN	1059
S	2740	GGAUGUCGGGAGACCUAGA	832	GGAUGUCGGGAGACCUAGANN	1060
AS	2740	UCUAGGUCUCCCGACAUCC	833	UCUAGGUCUCCCGACAUCCNN	1061
S	2741	GAUGUCGGGAGACCUAGAU	834	GAUGUCGGGAGACCUAGAUNN	1062
AS	2741	AUCUAGGUCUCCCGACAUC	835	AUCUAGGUCUCCCGACAUCNN	1063
S	2743	UGUCGGGAGACCUAGAUGA	836	UGUCGGGAGACCUAGAUGANN	1064
AS	2743	UCAUCUAGGUCUCCCGACA	837	UCAUCUAGGUCUCCCGACANN	1065
S	2768	CGGGUGCAAUACUAGCUAA	838	CGGGUGCAAUACUAGCUAANN	1066
AS	2768	UUAGCUAGUAUUGCACCCG	839	UUAGCUAGUAUUGCACCCGNN	1067
S	2771	GUGCAAUACUAGCUAAGGU	840	GUGCAAUACUAGCUAAGGUNN	1068

TABLE 3-continued

Sense and antisense strand sequences of human Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_013262.3, SEQ ID NO: 644)	Sequence (5' to 3')	SEQ ID NO:	Sequence with 3' dinucleotide overhang (5' to 3')	SEQ ID NO:
AS	2771	ACCUUAGCUAGUAUUGCAC	841	ACCUUAGCUAGUAUUGCACNN	1069
S	2772	UGCAAUACUAGCUAAGGUA	842	UGCAAUACUAGCUAAGGUANN	1070
AS	2772	UACCUUAGCUAGUAUUGCA	843	UACCUUAGCUAGUAUUGCANN	1071
S	2773	GCAAUACUAGCUAAGGUAA	844	GCAAUACUAGCUAAGGUAANN	1072
AS	2773	UUACCUUAGCUAGUAUUGC	845	UUACCUUAGCUAGUAUUGCNN	1073
S	2777	UACUAGCUAAGGUAAAGCU	846	UACUAGCUAAGGUAAAGCUNN	1074
AS	2777	AGCUUUACCUUAGCUAGUA	847	AGCUUUACCUUAGCUAGUANN	1075
S	2778	ACUAGCUAAGGUAAAGCUA	848	ACUAGCUAAGGUAAAGCUANN	1076
AS	2778	UAGCUUUACCUUAGCUAGU	849	UAGCUUUACCUUAGCUAGUNN	1077
S	2780	UAGCUAAGGUAAAGCUAGA	850	UAGCUAAGGUAAAGCUAGANN	1078
AS	2780	UCUAGCUUUACCUUAGCUA	851	UCUAGCUUUACCUUAGCUANN	1079
S	2852	AAUGUAGCAGUAAUGUGUU	852	AAUGUAGCAGUAAUGUGUUNN	1080
AS	2852	AACACAUUACUGCUACAUU	853	AACACAUUACUGCUACAUUNN	1081
S	2929	GGCACAUAUUAGCAUAUAA	854	GGCACAUAUUAGCAUAUAANN	1082
AS	2929	UUAUAUGCUAAUAUGUGCC	855	UUAUAUGCUAAUAUGUGCCNN	1083
S	2988	AAAUAAUGUUUCCACGUAA	856	AAAUAAUGUUUCCACGUAANN	1084
AS	2988	UUACGUGGAAACAUUAUUU	857	UUACGUGGAAACAUUAUUUNN	1085
S	2991	UAAUGUUUCCACGUAAAGA	858	UAAUGUUUCCACGUAAAGANN	1086
AS	2991	UCUUUACGUGGAAACAUUA	859	UCUUUACGUGGAAACAUUANN	1087
S	2992	AAUGUUUCCACGUAAAGAA	860	AAUGUUUCCACGUAAAGAANN	1088
AS	2992	UUCUUUACGUGGAAACAUU	861	UUCUUUACGUGGAAACAUUNN	1089
S	3006	AAGAACUCUGUUAUAUCCU	862	AAGAACUCUGUUAUAUCCUNN	1090
AS	3006	AGGAUAUAACAGAGUUCUU	863	AGGAUAUAACAGAGUUCUUNN	1091
S	3007	AGAACUCUGUUAUAUCCUA	864	AGAACUCUGUUAUAUCCUANN	1092
AS	3007	UAGGAUAUAACAGAGUUCU	865	UAGGAUAUAACAGAGUUCUNN	1093
S	3034	UGUCUUUUAUAUUCGGGAU	866	UGUCUUUUAUAUUCGGGAUNN	1094
AS	3034	AUCCCGAAUAUAAAAGACA	867	AUCCCGAAUAUAAAAGACANN	1095
S	3035	GUCUUUUAUAUUCGGGAUA	868	GUCUUUUAUAUUCGGGAUANN	1096
AS	3035	UAUCCCGAAUAUAAAAGAC	869	UAUCCCGAAUAUAAAAGACNN	1097
S	3036	UCUUUUAUAUUCGGGAUAA	870	UCUUUUAUAUUCGGGAUAANN	1098
AS	3036	UUAUCCCGAAUAUAAAAGA	871	UUAUCCCGAAUAUAAAAGANN	1099
S	3037	CUUUUAUAUUCGGGAUAAU	872	CUUUUAUAUUCGGGAUAAUNN	1100
AS	3037	AUUAUCCCGAAUAUAAAAG	873	AUUAUCCCGAAUAUAAAAGNN	1101
S	3049	GGAUAAUAAAGACUUUAAA	874	GGAUAAUAAAGACUUUAAANN	1102
AS	3049	UUUAAAGUCUUUAUUAUCC	875	UUUAAAGUCUUUAUUAUCCNN	1103

TABLE 4

Sense and antisense strand sequences of mouse and rat Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_153789.3, SEQ ID NO: 645)	Sequence (5' to 3')	SEQ ID NO:	Sequence with 3' dinucleotide overhang (5' to 3')	SEQ ID NO:
S	14	GAGCGGCGCGGCCGUGUAG	168	GAGCGGCGCGGCCGUGUAGNN	234
AS	14	CUACACGGCCGCGCCGCUC	169	CUACACGGCCGCGCCGCUCNN	235
S	26	CGUGUAGCUCCCGGGAACU	170	CGUGUAGCUCCCGGGAACUNN	236
AS	26	AGUUCCCGGGAGCUACACG	171	AGUUCCCGGGAGCUACACGNN	237
S	218	GCUGUGCUAUGUGACGAGG	172	GCUGUGCUAUGUGACGAGGNN	238
AS	218	CCUCGUCACAUAGCACAGC	173	CCUCGUCACAUAGCACAGCNN	239
S	220	UGUGCUAUGUGACGAGGCC	174	UGUGCUAUGUGACGAGGCCNN	240
AS	220	GGCCUCGUCACAUAGCACA	175	GGCCUCGUCACAUAGCACANN	241
S	485	GCAGACAAGGCAUAUCUUU	176	GCAGACAAGGCAUAUCUUUNN	242
AS	485	AAAGAUAUGCCUUGUCUGC	177	AAAGAUAUGCCUUGUCUGCNN	243
S	764	GAACUACGGCAUAGAGUGG	178	GAACUACGGCAUAGAGUGGNN	244
AS	764	CCACUCUAUGCCGUAGUUC	179	CCACUCUAUGCCGUAGUUCNN	245
S	766	ACUACGGCAUAGAGUGGCA	180	ACUACGGCAUAGAGUGGCANN	246
AS	766	UGCCACUCUAUGCCGUAGU	181	UGCCACUCUAUGCCGUAGUNN	247
S	857	GGACUUUAGCCCUAUUAAC	182	GGACUUUAGCCCUAUUAACNN	248
AS	857	GUUAAUAGGGCUAAAGUCC	183	GUUAAUAGGGCUAAAGUCCNN	249
S	858	GACUUUAGCCCUAUUAACA	184	GACUUUAGCCCUAUUAACANN	250
AS	858	UGUUAAUAGGGCUAAAGUC	185	UGUUAAUAGGGCUAAAGUCNN	251
S	867	CCUAUUAACAGGAUAGCUU	186	CCUAUUAACAGGAUAGCUUNN	252
AS	867	AAGCUAUCCUGUUAAUAGG	187	AAGCUAUCCUGUUAAUAGGNN	253
S	869	UAUUAACAGGAUAGCUUAU	188	UAUUAACAGGAUAGCUUAUNN	254
AS	869	AUAAGCUAUCCUGUUAAUA	189	AUAAGCUAUCCUGUUAAUANN	255
S	870	AUUAACAGGAUAGCUUAUC	190	AUUAACAGGAUAGCUUAUCNN	256
AS	870	GAUAAGCUAUCCUGUUAAU	191	GAUAAGCUAUCCUGUUAAUNN	257
S	871	UUAACAGGAUAGCUUAUCC	192	UUAACAGGAUAGCUUAUCCNN	258
AS	871	GGAUAAGCUAUCCUGUUAA	193	GGAUAAGCUAUCCUGUUAANN	259
S	873	AACAGGAUAGCUUAUCCUG	194	AACAGGAUAGCUUAUCCUGNN	260
AS	873	CAGGAUAAGCUAUCCUGUU	195	CAGGAUAAGCUAUCCUGUUNN	261
S	875	CAGGAUAGCUUAUCCUGUG	196	CAGGAUAGCUUAUCCUGUGNN	262
AS	875	CACAGGAUAAGCUAUCCUG	197	CACAGGAUAAGCUAUCCUGNN	263
S	919	AGAAUGUCUACUUGACCGU	198	AGAAUGUCUACUUGACCGUNN	264
AS	919	ACGGUCAAGUAGACAUUCU	199	ACGGUCAAGUAGACAUUCUNN	265
S	92	UGUCUACUUGACCGUCACC	200	UGUCUACUUGACCGUCACCNN	266
AS	923	GGUGACGGUCAAGUAGACA	201	GGUGACGGUCAAGUAGACANN	267
S	1815	UCAAGUAAAGGAGUAGAUA	202	UCAAGUAAAGGAGUAGAUANN	268
AS	1815	UAUCUACUCCUUUACUUGA	203	UAUCUACUCCUUUACUUGANN	269

TABLE 4-continued

Sense and antisense strand sequences of mouse and rat Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_153789.3, SEQ ID NO: 645)	Sequence (5' to 3')	SEQ ID NO:	Sequence with 3' dinucleotide overhang (5' to 3')	SEQ ID NO:
S	1856	GGCAACAUGGCCCAACCGU	204	GGCAACAUGGCCCAACCGUNN	270
AS	1856	ACGGUUGGGCCAUGUUGCC	205	ACGGUUGGGCCAUGUUGCCNN	271
S	1859	AACAUGGCCCAACCGUGGG	206	AACAUGGCCCAACCGUGGGNN	272
AS	1859	CCCACGGUUGGGCCAUGUU	207	CCCACGGUUGGGCCAUGUUNN	273
S	1861	CAUGGCCCAACCGUGGGCA	208	CAUGGCCCAACCGUGGGCANN	274
AS	1861	UGCCCACGGUUGGGCCAUG	209	UGCCCACGGUUGGGCCAUGNN	275
S	1968	UUGUAUGGUCAUGGAGCGC	210	UUGUAUGGUCAUGGAGCGCNN	276
AS	1968	GCGCUCCAUGACCAUACAA	211	GCGCUCCAUGACCAUACAANN	277
S	1969	UGUAUGGUCAUGGAGCGCU	212	UGUAUGGUCAUGGAGCGCUNN	278
AS	1969	AGCGCUCCAUGACCAUACA	213	AGCGCUCCAUGACCAUACANN	279
S	2512	UCUACAGCCUUAUAGGUUU	214	UCUACAGCCUUAUAGGUUUNN	280
AS	2512	AAACCUAUAAGGCUGUAGA	215	AAACCUAUAAGGCUGUAGANN	281
S	2695	GAAGCUAGUGAGCUAGGGG	216	GAAGCUAGUGAGCUAGGGGNN	282
AS	2695	CCCCUAGCUCACUAGCUUC	217	CCCCUAGCUCACUAGCUUCNN	283
S	2744	CCUCAUCGGGUGCAAUACU	218	CCUCAUCGGGUGCAAUACUNN	284
AS	2744	AGUAUUGCACCCGAUGAGG	219	AGUAUUGCACCCGAUGAGGNN	285
S	2745	CUCAUCGGGUGCAAUACUA	220	CUCAUCGGGUGCAAUACUANN	286
AS	2745	UAGUAUUGCACCCGAUGAG	221	UAGUAUUGCACCCGAUGAGNN	287
S	2746	UCAUCGGGUGCAAUACUAG	222	UCAUCGGGUGCAAUACUAGNN	288
AS	2746	CUAGUAUUGCACCCGAUGA	223	CUAGUAUUGCACCCGAUGANN	289
S	2747	CAUCGGGUGCAAUACUAGC	224	CAUCGGGUGCAAUACUAGCNN	290
AS	2747	GCUAGUAUUGCACCCGAUG	225	GCUAGUAUUGCACCCGAUGNN	291
S	2748	AUCGGGUGCAAUACUAGCU	226	AUCGGGUGCAAUACUAGCUNN	292
AS	2748	AGCUAGUAUUGCACCCGAU	227	AGCUAGUAUUGCACCCGAUNN	293
S	2749	UCGGGUGCAAUACUAGCUA	228	UCGGGUGCAAUACUAGCUANN	294
AS	2749	UAGCUAGUAUUGCACCCGA	229	UAGCUAGUAUUGCACCCGANN	295
S	2918	AUUAGCAUAUAAGCCUUUA	230	AUUAGCAUAUAAGCCUUUANN	296
AS	2918	UAAAGGCUUAUAUGCUAAU	231	UAAAGGCUUAUAUGCUAAUNN	297
S	2919	UUAGCAUAUAAGCCUUUAU	232	UUAGCAUAUAAGCCUUUAUNN	298
AS	2919	AUAAAGGCUUAUAUGCUAA	233	AUAAAGGCUUAUAUGCUAANN	299

TABLE 5

Sense and antisense strand sequences of human Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_013262.3, SEQ ID NO: 644)	Sequence with 3'deoxythimidine overhang (phosphodiester linkage)(5' to 3')	SEQ ID NO:	Sequence with 3'deoxythimidine overhang (phosphorothioate linkage)(5' to 3')	SEQ ID NO:
S	240	GCUGUGUUAUGUGACGAGGdT dT	300	GCUGUGUUAUGUGACGAGGdTs dT	374
AS	240	CCUCGUCACAUAACACAGCdT dT	301	CCUCGUCACAUAACACAGCdTs dT	375
S	241	CUGUGUUAUGUGACGAGGCdT dT	302	CUGUGUUAUGUGACGAGGdTs dTC	376
AS	241	GCCUCGUCACAUAACACAGdT dT	303	GCCUCGUCACAUAACACAGdTs dT	377
S	244	UGUUAUGUGACGAGGCCGGdT dT	304	UGUUAUGUGACGAGGCCGGdTs dT	378
AS	244	CCGGCCUCGUCACAUAACAdT dT	305	CCGGCCUCGUCACAUAACAdTs dT	379
S	245	GUUAUGUGACGAGGCCGGAdT dT	306	GUUAUGUGACGAGGCCGGAdTs dT	380
AS	245	UCCGGCCUCGUCACAUAACdT dT	307	UCCGGCCUCGUCACAUAACdTs dT	381
S	246	UUAUGUGACGAGGCCGGACdT dT	308	UUAUGUGACGAGGCCGGACdTs dT	382
AS	246	GUCCGGCCUCGUCACAUAAdT dT	309	GUCCGGCCUCGUCACAUAAdTs dT	383
S	247	UAUGUGACGAGGCCGGACGdT dT	310	UAUGUGACGAGGCCGGACGdTs dT	384
AS	247	CGUCCGGCCUCGUCACAUAdT dT	311	CGUCCGGCCUCGUCACAUAdTs dT	385
S	248	AUGUGACGAGGCCGGACGCdT dT	312	AUGUGACGAGGCCGGACGCdTs dT	386
AS	248	GCGUCCGGCCUCGUCACAUdT dT	313	GCGUCCGGCCUCGUCACAUdTs dT	387
S	249	UGUGACGAGGCCGGACGCGdT dT	314	UGUGACGAGGCCGGACGCGdTs dT	388
AS	249	CGCGUCCGGCCUCGUCACAdT dT	315	CGCGUCCGGCCUCGUCACAdTs dT	389
S	290	AGGCGAAAGCCAACGGCGAdT dT	316	AGGCGAAAGCCAACGGCGAdTs dT	390
AS	290	UCGCCGUUGGCUUUCGCCUdT dT	317	UCGCCGUUGGCUUUCGCCUdTs dT	391
S	291	GGCGAAAGCCAACGGCGAGdT dT	318	GGCGAAAGCCAACGGCGAGdTs dT	392
AS	291	CUCGCCGUUGGCUUUCGCCdT dT	319	CUCGCCGUUGGCUUUCGCCdTs dT	393
S	331	AGGCGACUGGGAAUCAUAGdT dT	320	AGGCGACUGGGAAUCAUAGdTs dT	394
AS	331	CUAUGAUUCCCAGUCGCCUdT dT	321	CUAUGAUUCCCAGUCGCCUdTs dT	395
S	332	GGCGACUGGGAAUCAUAGAdT dT	322	GGCGACUGGGAAUCAUAGAdTs dT	396
AS	332	UCUAUGAUUCCCAGUCGCCdTs	323	UCUAUGAUUCCCAGUCGCC dT	397

TABLE 5-continued

Sense and antisense strand sequences of human Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_013262.3, SEQ ID NO: 644)	Sequence with 3'deoxythimidine overhang (phosphodiester linkage)(5' to 3')	SEQ ID NO:	Sequence with 3'deoxythimidine overhang (phosphorothioate linkage)(5' to 3')	SEQ ID NO:
S	333	GCGACUGGGAAUCAUAGAAdTdT	324	GCGACUGGGAAUCAUAGAAdTsdT	398
AS	333	UUCUAUGAUUCCCAGUCGCdTdT	325	UUCUAUGAUUCCCAGUCGCdTsdT	399
S	368	UGCAGUUUACGGGUAGCAAdTdT	326	UGCAGUUUACGGGUAGCAAdTsdT	400
AS	368	UUGCUACCCGUAAACUGCAdTdT	327	UUGCUACCCGUAAACUGCAdTsdT	401
S	369	GCAGUUUACGGGUAGCAAAdTdT	328	GCAGUUUACGGGUAGCAAAdTsdT	402
AS	369	UUUGCUACCCGUAAACUGCdTdT	329	UUUGCUACCCGUAAACUGCdTsdT	403
S	370	CAGUUUACGGGUAGCAAAGdTdT	330	CAGUUUACGGGUAGCAAAGdTsdT	404
AS	370	CUUUGCUACCCGUAAACUGdTdT	331	CUUUGCUACCCGUAAACUGdTsdT	405
S	371	AGUUUACGGGUAGCAAAGGdTdT	332	AGUUUACGGGUAGCAAAGGdTsdT	406
AS	371	CCUUUGCUACCCGUAAACUdTdT	333	CCUUUGCUACCCGUAAACUdTsdT	407
S	372	GUUUACGGGUAGCAAAGGUdTdT	334	GUUUACGGGUAGCAAAGGUdTsdT	408
AS	372	ACCUUUGCUACCCGUAAACdTdT	335	ACCUUUGCUACCCGUAAACdTsdT	409
S	373	UUUACGGGUAGCAAAGGUGdTdT	336	UUUACGGGUAGCAAAGGUGdTsdT	410
AS	373	CACCUUUGCUACCCGUAAAdTdT	337	CACCUUUGCUACCCGUAAAdTsdT	411
S	386	AAGGUGAAAGUUUAUGGCUdTdT	338	AAGGUGAAAGUUUAUGGCUdTsdT	412
AS	386	AGCCAUAAACUUUCACCUUdTdT	339	AGCCAUAAACUUUCACCUUdTsdT	413
S	387	AGGUGAAAGUUUAUGGCUAdTdT	340	AGGUGAAAGUUUAUGGCUAdTsdT	414
AS	387	UAGCCAUAAACUUUCACCUdTdT	341	UAGCCAUAAACUUUCACCUdTsdT	415
S	388	GGUGAAAGUUUAUGGCUAAdTdT	342	GGUGAAAGUUUAUGGCUAAdTsdT	416
AS	388	UUAGCCAUAAACUUUCACCdTdT	343	UUAGCCAUAAACUUUCACCdTsdT	417
S	393	AAGUUUAUGGCUAAACCUGdTdT	344	AAGUUUAUGGCUAAACCUGdTsdT	418
AS	393	CAGGUUUAGCCAUAAACUUdTdT	345	CAGGUUUAGCCAUAAACUUdTsdT	419
S	395	GUUUAUGGCUAAACCUGAGdTdT	346	GUUUAUGGCUAAACCUGAGdTsdT	420
AS	395	CUCAGGUUUAGCCAUAAACdTdT	347	CUCAGGUUUAGCCAUAAACdTsdT	421

TABLE 5-continued

Sense and antisense strand sequences of human Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_013262.3, SEQ ID NO: 644)	Sequence with 3'deoxythimidine overhang (phosphodiester linkage)(5' to 3')	SEQ ID NO:	Sequence with 3'deoxythimidine overhang (phosphorothioate linkage)(5' to 3')	SEQ ID NO:
S	434	UGGAUGGGCUAGCCCCUUAdTdT	348	UGGAUGGGCUAGCCCCUUAdTsdT	422
AS	434	UAAGGGGCUAGCCCAUCCAdTdT	349	UAAGGGGCUAGCCCAUCCAdTsdT	423
S	435	GGAUGGGCUAGCCCCUUACdTdT	350	GGAUGGGCUAGCCCCUUACdTsdT	424
AS	435	GUAAGGGGCUAGCCCAUCCdTdT	351	GUAAGGGGCUAGCCCAUCCdTsdT	425
S	438	UGGGCUAGCCCCUUACAGGdTdT	352	UGGGCUAGCCCCUUACAGGdTsdT	426
AS	438	CCUGUAAGGGGCUAGCCCAdTdT	353	CCUGUAAGGGGCUAGCCCAdTsdT	427
S	439	GGGCUAGCCCCUUACAGGCdTdT	354	GGGCUAGCCCCUUACAGGCdTsdT	428
AS	439	GCCUGUAAGGGGCUAGCCCdTdT	355	GCCUGUAAGGGGCUAGCCCdTsdT	429
S	440	GGCUAGCCCCUUACAGGCUdTdT	356	GGCUAGCCCCUUACAGGCUdTsdT	430
AS	440	AGCCUGUAAGGGGCUAGCCdTdT	357	AGCCUGUAAGGGGCUAGCCdTsdT	431
S	444	AGCCCCUUACAGGCUUAAAdTdT	358	AGCCCCUUACAGGCUUAAAdTsdT	432
AS	444	UUUAAGCCUGUAAGGGGCUdTdT	359	UUUAAGCCUGUAAGGGGCUdTsdT	433
S	446	CCCCUUACAGGCUUAAACUdTdT	360	CCCCUUACAGGCUUAAACUdTsdT	434
AS	446	AGUUUAAGCCUGUAAGGGGdTdT	361	AGUUUAAGCCUGUAAGGGGdTsdT	435
S	498	CUUACAGGAGCAGACUAGGdTdT	362	CUUACAGGAGCAGACUAGGdTsdT	436
AS	498	CCUAGUCUGCUCCUGUAAGdTdT	363	CCUAGUCUGCUCCUGUAAGdTsdT	437
S	508	CAGACUAGGCAUAUCUUUUdTdT	364	CAGACUAGGCAUAUCUUUUdTsdT	438
AS	508	AAAAGAUAUGCCUAGUCUGdTdT	365	AAAAGAUAUGCCUAGUCUGdTsdT	439
S	640	ACUGCCAAGUAUAACUAUGdTdT	366	ACUGCCAAGUAUAACUAUGdTsdT	440
AS	640	CAUAGUUAUACUUGGCAGUdTdT	367	CAUAGUUAUACUUGGCAGUdTsdT	441
S	763	UUGCAGAUUGUGUCGGCAAdTdT	368	UUGCAGAUUGUGUCGGCAAdTsdT	442
AS	763	UUGCCGACACAAUCUGCAAdTdT	369	UUGCCGACACAAUCUGCAAdTsdT	443
S	764	UGCAGAUUGUGUCGGCAAUdTdT	370	UGCAGAUUGUGUCGGCAAUdTsdT	444
AS	764	AUUGCCGACACAAUCUGCAdTdT	371	AUUGCCGACACAAUCUGCAdTsdT	445

TABLE 5-continued

Sense and antisense strand sequences of human Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_013262.3, SEQ ID NO: 644)	Sequence with 3'deoxythimidine overhang (phosphodiester linkage)(5' to 3')	SEQ ID NO:	Sequence with 3'deoxythimidine overhang (phosphorothioate linkage)(5' to 3')	SEQ ID NO:
S	765	GCAGAUUGUGUCGGCAAUGdT dT	372	GCAGAUUGUGUCGGCAAUGdTs dT	446
AS	765	CAUUGCCGACACAAUCUGCdT dT	373	CAUUGCCGACACAAUCUGCdTs dT	447

TABLE 6

Sense and antisense strand sequences of mouse/rat Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_153789.3, SEQ ID NO: 645)	Sequence with 3'deoxythimidine overhang (phosphodiester linkage)(5' to 3')	SEQ ID NO:	Sequence with 3'deoxythimidine overhang (phosphorothioate linkage)(5' to 3')	SEQ ID NO:
S	14	GAGCGGCGCGGCCGUGUAGdT dT	448	GAGCGGCGCGGCCGUGUAGdTs dT	514
AS	14	CUACACGGCCGCGCCGCUCdT dT	449	CUACACGGCCGCGCCGCUCdTs dT	515
S	26	CGUGUAGCUCCCGGGAACUdT dT	450	CGUGUAGCUCCCGGGAACUdTs dT	516
AS	26	AGUUCCCGGGAGCUACACGdT dT	451	AGUUCCCGGGAGCUACACGdTs dT	517
S	218	GCUGUGCUAUGUGACGAGGdT dT	452	GCUGUGCUAUGUGACGAGGdTs dT	518
AS	218	CCUCGUCACAUAGCACAGCdT dT	453	CCUCGUCACAUAGCACAGCdTs dT	519
S	220	UGUGCUAUGUGACGAGGCCdT dT	454	UGUGCUAUGUGACGAGGCCdTs dT	520
AS	220	GGCCUCGUCACAUAGCACAdT dT	455	GGCCUCGUCACAUAGCACAdTs dT	521
S	485	GCAGACAAGGCAUAUCUUUdT dT	456	GCAGACAAGGCAUAUCUUUdTs dT	522
AS	485	AAAGAUAUGCCUUGUCUGCdT dT	457	AAAGAUAUGCCUUGUCUGCdTs dT	523
S	764	GAACUACGGCAUAGAGUGGdT dT	458	GAACUACGGCAUAGAGUGGdTs dT	524
AS	764	CCACUCUAUGCCGUAGUUCdT dT	459	CCACUCUAUGCCGUAGUUCdTs dT	525
S	766	ACUACGGCAUAGAGUGGCAdT dT	460	ACUACGGCAUAGAGUGGCAdTs dT	526
AS	766	UGCCACUCUAUGCCGUAGUdT dT	461	UGCCACUCUAUGCCGUAGUdTs dT	527
S	857	GGACUUUAGCCCUAUUAACdT dT	462	GGACUUUAGCCCUAUUAACdTs dT	528
AS	857	GUUAAUAGGGCUAAAGUCCdT dT	463	GUUAAUAGGGCUAAAGUCCdTs dT	529
S	858	GACUUUAGCCCUAUUAACAdT dT	464	GACUUUAGCCCUAUUAACAdTs dT	530
AS	858	UGUUAAUAGGGCUAAAGUCdT dT	465	UGUUAAUAGGGCUAAAGUCdTs dT	531

TABLE 6-continued

Sense and antisense strand sequences of mouse/rat Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_153789.3, SEQ ID NO: 645)	Sequence with 3'deoxythimidine overhang (phosphodiester linkage)(5' to 3')	SEQ ID NO:	Sequence with 3'deoxythimidine overhang (phosphorothioate linkage)(5' to 3')	SEQ ID NO:
S	867	CCUAUUAACAGGAUAGCUUdTdT	466	CCUAUUAACAGGAUAGCUUdTsdT	532
AS	867	AAGCUAUCCUGUUAAUAGGdTdT	467	AAGCUAUCCUGUUAAUAGGdTsdT	533
S	869	UAUUAACAGGAUAGCUUAUdTdT	468	UAUUAACAGGAUAGCUUAUdTsdT	534
AS	869	AUAAGCUAUCCUGUUAAUAdTdT	469	AUAAGCUAUCCUGUUAAUAdTsdT	535
S	870	AUUAACAGGAUAGCUUAUCdTdT	470	AUUAACAGGAUAGCUUAUCdTsdT	536
AS	870	GAUAAGCUAUCCUGUUAAUdTdT	471	GAUAAGCUAUCCUGUUAAUdTsdT	537
S	871	UUAACAGGAUAGCUUAUCCdTdT	472	UUAACAGGAUAGCUUAUCCdTsdT	538
AS	871	GGAUAAGCUAUCCUGUUAAdTdT	473	GGAUAAGCUAUCCUGUUAAdTsdT	539
S	873	AACAGGAUAGCUUAUCCUGdTdT	474	AACAGGAUAGCUUAUCCUGdTsdT	540
AS	873	CAGGAUAAGCUAUCCUGUUdTdT	475	CAGGAUAAGCUAUCCUGUUdTsdT	541
S	875	CAGGAUAGCUUAUCCUGUGdTdT	476	CAGGAUAGCUUAUCCUGUGdTsdT	542
AS	875	CACAGGAUAAGCUAUCCUGdTdT	477	CACAGGAUAAGCUAUCCUGdTsdT	543
S	919	AGAAUGUCUACUUGACCGUdTdT	478	AGAAUGUCUACUUGACCGUdTsdT	544
AS	919	ACGGUCAAGUAGACAUUCUdTdT	479	ACGGUCAAGUAGACAUUCUdTsdT	545
S	92	UGUCUACUUGACCGUCACCdTdT	480	UGUCUACUUGACCGUCACCdTsdT	546
AS	923	GGUGACGGUCAAGUAGACAdTdT	481	GGUGACGGUCAAGUAGACAdTsdT	547
S	1815	UCAAGUAAAGGAGUAGAUAdTdT	482	UCAAGUAAAGGAGUAGAUAdTsdT	548
AS	1815	UAUCUACUCCUUUACUUGAdTdT	483	UAUCUACUCCUUUACUUGAdTsdT	549
S	1856	GGCAACAUGGCCCAACCGUdTdT	484	GGCAACAUGGCCCAACCGUdTsdT	550
AS	1856	ACGGUUGGGCCAUGUUGCCdTdT	485	ACGGUUGGGCCAUGUUGCCdTsdT	551
S	1859	AACAUGGCCCAACCGUGGGdTdT	486	AACAUGGCCCAACCGUGGGdTsdT	552
AS	1859	CCCACGGUUGGGCCAUGUUdTdT	487	CCCACGGUUGGGCCAUGUUdTsdT	553
S	1861	CAUGGCCCAACCGUGGGCAdTdT	488	CAUGGCCCAACCGUGGGCAdTsdT	554
AS	1861	UGCCCACGGUUGGGCCAUGdTdT	489	UGCCCACGGUUGGGCCAUGdTsdT	555

TABLE 6-continued

Sense and antisense strand sequences of mouse/rat Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_153789.3, SEQ ID NO: 645)	Sequence with 3'deoxythimidine overhang (phosphodiester linkage)(5' to 3')	SEQ ID NO:	Sequence with 3'deoxythimidine overhang (phosphorothioate linkage)(5' to 3')	SEQ ID NO:
S	1968	UUGUAUGGUCAUGGAGCGCdTdT	490	UUGUAUGGUCAUGGAGCGCdTsdT	556
AS	1968	GCGCUCCAUGACCAUACAAdTdT	491	GCGCUCCAUGACCAUACAAdTsdT	557
S	1969	UGUAUGGUCAUGGAGCGCUdTdT	492	UGUAUGGUCAUGGAGCGCUdTsdT	558
AS	1969	AGCGCUCCAUGACCAUACAdTdT	493	AGCGCUCCAUGACCAUACAdTsdT	559
S	2512	UCUACAGCCUUAUAGGUUUdTdT	494	UCUACAGCCUUAUAGGUUUdTsdT	560
AS	2512	AAACCUAUAAGGCUGUAGAdTdT	495	AAACCUAUAAGGCUGUAGAdTsdT	561
S	2695	GAAGCUAGUGAGCUAGGGGdTdT	496	GAAGCUAGUGAGCUAGGGGdTsdT	562
AS	2695	CCCCUAGCUCACUAGCUUCdTdT	497	CCCCUAGCUCACUAGCUUCdTsdT	563
S	2744	CCUCAUCGGGUGCAAUACUdTdT	498	CCUCAUCGGGUGCAAUACUdTsdT	564
AS	2744	AGUAUUGCACCCGAUGAGGdTdT	499	AGUAUUGCACCCGAUGAGGdTsdT	565
S	2745	CUCAUCGGGUGCAAUACUAdTdT	500	CUCAUCGGGUGCAAUACUAdTsdT	566
AS	2745	UAGUAUUGCACCCGAUGAGdTdT	501	UAGUAUUGCACCCGAUGAGdTsdT	567
S	2746	UCAUCGGGUGCAAUACUAGdTdT	502	UCAUCGGGUGCAAUACUAGdTsdT	568
AS	2746	CUAGUAUUGCACCCGAUGAdTdT	503	CUAGUAUUGCACCCGAUGAdTsdT	569
S	2747	CAUCGGGUGCAAUACUAGCdTdT	504	CAUCGGGUGCAAUACUAGCdTsdT	570
AS	2747	GCUAGUAUUGCACCCGAUGdTdT	505	GCUAGUAUUGCACCCGAUGdTsdT	571
S	2748	AUCGGGUGCAAUACUAGCUdTdT	506	AUCGGGUGCAAUACUAGCUdTsdT	572
AS	2748	AGCUAGUAUUGCACCCGAUdTdT	507	AGCUAGUAUUGCACCCGAUdTsdT	573
S	2749	UCGGGUGCAAUACUAGCUAdTdT	508	UCGGGUGCAAUACUAGCUAdTsdT	574
AS	2749	UAGCUAGUAUUGCACCCGAdTdT	509	UAGCUAGUAUUGCACCCGAdTsdT	575
S	2918	AUUAGCAUAUAAGCCUUUAdTdT	510	AUUAGCAUAUAAGCCUUUAdTsdT	576
AS	2918	UAAAGGCUUAUAUGCUAAUdTdT	511	UAAAGGCUUAUAUGCUAAUdTsdT	577

TABLE 6-continued

Sense and antisense strand sequences of mouse/rat Mylip/Idol dsRNAs

Strand ID (S = sense; AS = antisense)	position of 5' base on transcript (NM_153789.3, SEQ ID NO: 645)	Sequence with 3'deoxythimidine overhang (phosphodiester linkage)(5' to 3')	SEQ ID NO:	Sequence with 3'deoxythimidine overhang (phosphorothioate linkage)(5' to 3')	SEQ ID NO:
S	2919	UUAGCAUAUAAGCCUUUAUdTdT	512	UUAGCAUAUAAGCCUUUAUdTsdT	578
AS	2919	AUAAAGGCUUAUAUGCUAAdTdT	513	AUAAAGGCUUAUAUGCUAAdTsdT	579

TABLE 7

Chemically modified sense and antisense strand sequences of Mylip/Idol dsRNAs

Strand ID (S = sense; AS = anti-sense)	Position of 5' base on transcript (NM_001098791.1, SEQ ID NO: 1299)	Sequence (5' to 3')	SEQ ID NO:
S		GAGcGGcGcGGccGuGuAGdTsdT	580
AS		CuAcACGGCCGCGCCGCUCdTsdT	581
S		cGuGuAGcucccGGGAAcudTsdT	582
AS		AGUUCCCGGGAGCuAcACGdTsdT	583
S		GcuGuGcuAuGuGAcGAGGdTsdT	584
AS		CCUCGUcAcAuAGcAcAGCdTsdT	585
S		uGuGcuAuGuGAcGAGGccdTsdT	586
AS		GGCCUCGUcAcAuAGcAcAdTsdT	587
S		GcAGAcAAGGcAuAucuuudTsdT	588
AS		AAAGAuAUGCCUUGUCUGCdTsdT	589
S		GAAcuAcGGcAuAGAGuGGdTsdT	590
AS		CcACUCuAUGCCGuAGUUCdTsdT	591
S		AcuAcGGcAuAGAGuGGcAdTsdT	592
AS		UGCcACUCuAUGCCGuAGUdTsdT	593
S		GGAcuuuAGcccuAuuAAcdTsdT	594
AS		GUuAAuAGGGCuAAAGUCCdTsdT	595
S		GAcuuuAGcccuAuuAAcAdTsdT	596
AS		UGUuAAuAGGGCuAAAGUCdTsdT	597
S		ccuAuuAAcAGGAuAGcuudTsdT	598
AS		AAGCuAUCCUGUuAAuAGGdTsdT	599
S		uAuuAAcAGGAuAGcuuAudTsdT	600
AS		AuAAGCuAUCCUGUuAAuAdTsdT	601
S		AuuAAcAGGAuAGcuuAucdTsdT	602
AS		GAuAAGCuAUCCUGUuAAUdTsdT	603
S		uuAAcAGGAuAGcuuAuccdTsdT	604

TABLE 7-continued

Chemically modified sense and antisense strand sequences of Mylip/Idol dsRNAs

Strand ID (S = sense; AS = anti-sense)	Position of 5' base on transcript (NM_001098791.1, SEQ ID NO: 1299)	Sequence (5' to 3')	SEQ ID NO:
AS		GGAuAAGCuAUCCUGUuAAdTsdT	605
S		cAGGAuAGcuuAuccuGuGdTsdT	606
AS		cAcAGGAuAAGCuAUCCUGdTsdT	607
S		AGAAuGucuAcuuGAccGudTsdT	608
AS		ACGGUcAAGuAGAcAUUCUdTsdT	609
S		uGucuAcuuGAccGucAccdTsdT	610
AS		GGUGACGGUcAAGuAGAcAdTsdT	611
S		ucAAGuAAAGGAGuAGAuAdTsdT	612
AS		uAUCuACUCCUUuACUUGAdTsdT	613
S		GGcAAcAuGGcccAAccGudTsdT	614
AS		ACGGUUGGGCcAUGUUGCCdTsdT	615
S		AAcAuGGcccAAccGuGGGdTsdT	616
AS		CCcACGGUUGGGCcAUGUUdTsdT	617
S		cAuGGcccAAccGuGGGcAdTsdT	618
AS		UGCCcACGGUUGGGCcAUGdTsdT	619
S		uuGuAuGGucAuGGAGcGcdTsdT	620
AS		GCGCUCcAUGACcAuAcAAdTsdT	621
S		uGuAuGGucAuGGAGcGcudTsdT	622
AS		AGCGCUCcAUGACcAuAcAdTsdT	623
S		ucuAcAGccuuAuAGGuuudTsdT	624
AS		AAACCuAuAAGGCUGuAGAdTsdT	625
S		GAAGcuAGuGAGcuAGGGGdTsdT	626
AS		CCCCuAGCUcACuAGCUUCdTsdT	627
S		ccucAucGGGuGcAAuAcudTsdT	628

TABLE 7-continued

Chemically modified sense and antisense strand sequences of Mylip/Idol dsRNAs

Strand ID (S = sense; AS = anti-sense)	Position of 5' base on transcript (NM_001098791.1, SEQ ID NO: 1299)	Sequence (5' to 3')	SEQ ID NO:
AS		AGuAUUGcACCCGAUGAGGdTsdT	629
S		cucAucGGGuGcAAuAcuAdTsdT	630
AS		uAGuAUUGcACCCGAUGAGdTsdT	631
S		ucAucGGGuGcAAuAcuAGdTsdT	632
AS		CuAGuAUUGcACCCGAUGAdTsdT	633
S		cAucGGGuGcAAuAcuAGcdTsdT	634
AS		GCuAGuAUUGcACCCGAUGdTsdT	635
S		AucGGGuGcAAuAcuAGcudTsdT	636
AS		AGCuAGuAUUGcACCCGAUdTsdT	637
S		ucGGGuGcAAuAcuAGcuAdTsdT	638
AS		uAGCuAGuAUUGcACCCGAdTsdT	639
S		AuuAGcAuAuAAGccuuuAdTsdT	640
AS		uAAAGGCUuAuAUGCuAAUdTsdT	641
S		AAcAGGAuAGcuuAuccuGdTsdT	642
AS		cAGGAuAAGCuAUCCUGUUdTsdT	643

Synthesis of Mylip/Idol Sequences

Mylip/Idol iRNA sequences were synthesized on a MerMade 192 synthesizer at 1 μmol scale.

For all the sequences in Table 5, 'endolight' chemistry was applied as detailed below.

All pyrimidines (cytosine and uridine) in the sense strand contained 2'-O-Methyl bases (2' O-Methyl C and 2'-O-Methyl U)

In the antisense strand, pyrimidines adjacent to (towards 5' position) ribo A nucleoside were replaced with their corresponding 2-O-Methyl nucleosides

A two base dTsdT extension at 3' end of both sense and anti sense sequences was introduced

The sequence file was converted to a text file to make it compatible for loading in the MerMade 192 synthesis software

Synthesis, Cleavage and Deprotection

The synthesis of Mylip/Idol sequences used solid supported oligonucleotide synthesis using phosphoramidite chemistry.

The synthesis of the above sequences was performed at 1 μm scale in 96 well plates. The amidite solutions were prepared at 0.1M concentration and ethyl thio tetrazole (0.6M in Acetonitrile) was used as activator.

The synthesized sequences were cleaved and deprotected in 96 well plates, using methylamine in the first step and fluoride reagent in the second step. The crude sequences were precipitated using acetone:ethanol (80:20) mix and the pellets were re-suspended in 0.02M sodium acetate buffer. Samples from each sequence were analyzed by LC-MS to confirm the identity, UV for quantification, and a selected set of samples were also analyzed by IEX chromatography to determine purity.

Purification and Desalting

All sequences were purified on AKTA explorer purification system using Source 15Q column. Sample injection and collection was performed in 96 well (1.8 mL-deep well) plates. A single peak corresponding to the full length sequence was collected in the eluent. The purified sequences were desalted on a Sephadex G25 column using AKTA purifier. The desalted Mylip/Idol sequences were analyzed for concentration (by UV measurement at A260) and purity (by ion exchange HPLC). The single strands were then submitted for annealing.

Other embodiments are in the claims.

SEQUENCE LISTING

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accuuugcua cccguaaac 19

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aaggugaaag uuuauggcu 19

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ggugaaaguu uauggcuaa 19

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guuuauggcu aaaccugag 19

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cucagguuua gccauaaac 19

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cagacuaggc auaucuuuu 19

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aaaagauaug ccuagucug 19

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cauaguuaua cuuggcagu 19

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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 90

ugcagauugu gucggcaau 19

<210> SEQ ID NO 91
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 91

auugccgaca caaucugca 19

<210> SEQ ID NO 92
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 92

gcagauugug ucggcaaug 19

<210> SEQ ID NO 93
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 93

cauugccgac acaaucugc 19

<210> SEQ ID NO 94
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 94

gcuguguuau gugacgaggn n 21

<210> SEQ ID NO 95
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 95

ccucgucaca uaacacagcn n 21

<210> SEQ ID NO 96
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 96

cuguguuaug ugacgaggcn n 21

<210> SEQ ID NO 97
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 97

gccucgucac auaacacagn n 21

<210> SEQ ID NO 98
<211> LENGTH: 21
<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 98

uguuauguga cgaggccggn n 21

<210> SEQ ID NO 99
<211> LENGTH: 21
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 99

ccggccucgu cacauaacan n 21

<210> SEQ ID NO 100
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 100

guuaugugac gaggccggan n 21

<210> SEQ ID NO 101
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 101

uccggccucg ucacauaacn n 21

<210> SEQ ID NO 102
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 102

uuaugugacg aggccggacn n 21

<210> SEQ ID NO 103
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 103

guccggccuc gucacauaan n 21

<210> SEQ ID NO 104
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 104

uaugugacga ggccggacgn n 21

<210> SEQ ID NO 105
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 105

cguccggccu cgucacauan n 21

<210> SEQ ID NO 106
<211> LENGTH: 21
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 106

augugacgag gccggacgcn n 21

<210> SEQ ID NO 107
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 107

gcguccggcc ucgucacaun n 21

<210> SEQ ID NO 108
<211> LENGTH: 21
<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 108

ugugacgagg ccggacgcgn n 21

<210> SEQ ID NO 109
<211> LENGTH: 21
<212> TYPE: DNA
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 109

cgcguccggc cucgucacan n 21

<210> SEQ ID NO 110
<211> LENGTH: 21

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<212> TYPE: DNA
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 110

aggcgaaagc caacggcgan n 21

<210> SEQ ID NO 111
<211> LENGTH: 21
<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 111

ucgccguugg cuuucgccun n 21

<210> SEQ ID NO 112
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 112

ggcgaaagcc aacggcgagn n 21

<210> SEQ ID NO 113
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 113

cucgccguug gcuuucgccn n 21

<210> SEQ ID NO 114

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<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 114

aggcgacugg gaaucauagn n 21

<210> SEQ ID NO 115
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 115

cuaugauucc cagucgccun n 21

<210> SEQ ID NO 116
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 116

ggcgacuggg aaucauagan n 21

<210> SEQ ID NO 117
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 117

ucuaugauuc ccagucgccn n 21

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<210> SEQ ID NO 118
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 118

gcgacuggga aucauagaan n 21

<210> SEQ ID NO 119
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 119

uucuaugauu cccagucgcn n 21

<210> SEQ ID NO 120
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 120

ugcaguuuac ggguagcaan n 21

<210> SEQ ID NO 121
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 121

uugcuacccg uaaacugcan n 21

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<210> SEQ ID NO 122
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 122

gcaguuuacg gguagcaaan n 21

<210> SEQ ID NO 123
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 123

uuugcuaccc guaaacugcn n 21

<210> SEQ ID NO 124
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 124

caguuuacgg guagcaaagn n 21

<210> SEQ ID NO 125
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 125

cuuugcuacc cguaaacugn n 21

<210> SEQ ID NO 126
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 126

aguuuacggg uagcaaaggn n 21

<210> SEQ ID NO 127
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 127

ccuuugcuac ccguaaacun n 21

<210> SEQ ID NO 128
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 128

guuuacgggu agcaaaggun n 21

<210> SEQ ID NO 129
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 129

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accuuugcua cccguaaacn n 21

<210> SEQ ID NO 130
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<212> TYPE: DNA
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 130

uuuacgggua gcaaaggugn n 21

<210> SEQ ID NO 131
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 131

caccuuugcu acccguaaan n 21

<210> SEQ ID NO 132
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 132

aaggugaaag uuuauggcun n 21

<210> SEQ ID NO 133
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 133

agccauaaac uuucaccuun n 21

<210> SEQ ID NO 134
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 134

aggugaaagu uuauggcuan n 21

<210> SEQ ID NO 135
<211> LENGTH: 21
<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 135

uagccauaaa cuuucaccun n 21

<210> SEQ ID NO 136
<211> LENGTH: 21
<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 136

ggugaaaguu uauggcuaan n 21

<210> SEQ ID NO 137
<211> LENGTH: 21
<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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<400> SEQUENCE: 137

uuagccauaa acuuucaccn n 21

<210> SEQ ID NO 138
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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aaguuuaugg cuaaaccugn n 21

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cagguuuagc cauaaacuun n 21

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guuuauggcu aaaccugagn n 21

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uggaugggcu agccccuuan n 21

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uaaggggcua gcccauccan n 21

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ggaugggcua gccccuuacn n 21

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ugggcuagcc ccuuacaggn n 21

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ccuguaaggg gcuagcccan n 21

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gggcuagccc cuuacaggcn n 21

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gccuguaagg ggcuagcccn n 21

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<400> SEQUENCE: 150

ggcuagcccc uuacaggcun n 21

<210> SEQ ID NO 151
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agccuguaag gggcuagccn n 21

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<400> SEQUENCE: 152

agccccuuac aggcuuaaan n 21

<210> SEQ ID NO 153
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 153

uuuaagccug uaaggggcun n 21

<210> SEQ ID NO 154
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<220> FEATURE:
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 154

ccccuuacag gcuuaaacun n 21

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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 155

aguuuaagcc uguaaggggn n 21

<210> SEQ ID NO 156
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 156

cuuacaggag cagacuaggn n 21

<210> SEQ ID NO 157
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 157

ccuagucugc uccuguaagn n 21

<210> SEQ ID NO 158
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cagacuaggc auaucuuuun n 21

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aaaagauaug ccuagucugn n 21

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<400> SEQUENCE: 160

acugccaagu auaacuaugn n 21

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<400> SEQUENCE: 161

cauaguuaua cuuggcagun n 21

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<400> SEQUENCE: 162

uugcagauug ugucggcaan n 21

<210> SEQ ID NO 163
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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uugccgacac aaucugcaan n 21

<210> SEQ ID NO 164
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<400> SEQUENCE: 164

ugcagauugu gucggcaaun n 21

<210> SEQ ID NO 165
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<400> SEQUENCE: 165

auugccgaca caaucugcan n 21

<210> SEQ ID NO 166
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<400> SEQUENCE: 166

gcagauugug ucggcaaugn n 21

<210> SEQ ID NO 167
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 167

cauugccgac acaaucugcn n 21

<210> SEQ ID NO 168
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 168

gagcggcgcg gccguguag 19

<210> SEQ ID NO 169
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 169

cuacacggcc gcgccgcuc 19

<210> SEQ ID NO 170

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<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 170

cguguagcuc ccgggaacu 19

<210> SEQ ID NO 171
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<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 171

aguucccggg agcuacacg 19

<210> SEQ ID NO 172
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 172

gcugugcuau gugacgagg 19

<210> SEQ ID NO 173
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<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 173

ccucgucaca uagcacagc 19

<210> SEQ ID NO 174
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<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 174

ugugcuaugu gacgaggcc 19

<210> SEQ ID NO 175
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<220> FEATURE:
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<400> SEQUENCE: 175

ggccucguca cauagcaca 19

<210> SEQ ID NO 176
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<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 176

gcagacaagg cauaucuuu 19

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<212> TYPE: RNA
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<400> SEQUENCE: 177

aaagauaugc cuugucugc 19

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<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 178

gaacuacggc auagagugg 19

<210> SEQ ID NO 179
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<400> SEQUENCE: 179

ccacucuaug ccguaguuc 19

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<212> TYPE: RNA
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<400> SEQUENCE: 180

acuacggcau agaguggca 19

<210> SEQ ID NO 181
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<400> SEQUENCE: 181

ugccacucua ugccguagu 19

<210> SEQ ID NO 182
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 182

ggacuuuagc ccuauuaac 19

<210> SEQ ID NO 183
<211> LENGTH: 19
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 183

guuaauaggg cuaaagucc 19

<210> SEQ ID NO 184
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<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 184

gacuuuagcc cuauuaaca 19

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<400> SEQUENCE: 185

uguuaauagg gcuaaaguc 19

<210> SEQ ID NO 186
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<212> TYPE: RNA
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<400> SEQUENCE: 186

ccuauuaaca ggauagcuu 19

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<400> SEQUENCE: 187

aagcuauccu guuaauagg 19

<210> SEQ ID NO 188
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<400> SEQUENCE: 188

uauuaacagg auagcuuau 19

<210> SEQ ID NO 189
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<400> SEQUENCE: 189

auaagcuauc cuguuaaua 19

<210> SEQ ID NO 190
<211> LENGTH: 19
<212> TYPE: RNA
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<400> SEQUENCE: 190

auuaacagga uagcuuauc 19

<210> SEQ ID NO 191
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<400> SEQUENCE: 191

gauaagcuau ccuguuaau 19

<210> SEQ ID NO 192
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<212> TYPE: RNA
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<400> SEQUENCE: 192

uuaacaggau agcuuaucc 19

<210> SEQ ID NO 193
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<400> SEQUENCE: 193

ggauaagcua uccuguuaa 19

<210> SEQ ID NO 194
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 194

aacaggauag cuuauccug 19

<210> SEQ ID NO 195
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<400> SEQUENCE: 195

caggauaagc uauccuguu 19

<210> SEQ ID NO 196
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<212> TYPE: RNA
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<400> SEQUENCE: 196

caggauagcu uauccugug 19

<210> SEQ ID NO 197
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<400> SEQUENCE: 197

cacaggauaa gcuauccug 19

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<400> SEQUENCE: 198

agaaugucua cuugaccgu 19

<210> SEQ ID NO 199
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<400> SEQUENCE: 199

acggucaagu agacauucu 19

<210> SEQ ID NO 200
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

oligonucleotide

<400> SEQUENCE: 200

ugucuacuug accgucacc 19

<210> SEQ ID NO 201
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 201

ggugacgguc aaguagaca 19

<210> SEQ ID NO 202
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 202

ucaaguaaag gaguagaua 19

<210> SEQ ID NO 203
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 203

uaucuacucc uuuacuuga 19

<210> SEQ ID NO 204
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 204

ggcaacaugg cccaaccgu 19

<210> SEQ ID NO 205
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 205

acgguugggc cauguugcc 19

<210> SEQ ID NO 206
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 206

aacauggccc aaccguggg 19

<210> SEQ ID NO 207
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 207

cccacgguug ggccauguu 19

<210> SEQ ID NO 208
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 208

cauggcccaa ccgugggca 19

<210> SEQ ID NO 209
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 209

ugcccacggu ugggccaug 19

<210> SEQ ID NO 210
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 210

uuguaugguc auggagcgc 19

<210> SEQ ID NO 211
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 211

gcgcuccaug accauacaa 19

<210> SEQ ID NO 212
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

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<400> SEQUENCE: 212

uguaugguca uggagcgcu 19

<210> SEQ ID NO 213
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 213

agcgcuccau gaccauaca 19

<210> SEQ ID NO 214
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 214

ucuacagccu uauagguuu 19

<210> SEQ ID NO 215
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 215

aaaccuauaa ggcuguaga 19

<210> SEQ ID NO 216
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 216

gaagcuagug agcuagggg 19

<210> SEQ ID NO 217
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 217

ccccuagcuc acuagcuuc 19

<210> SEQ ID NO 218
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 218

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ccucaucggg ugcaauacu 19

<210> SEQ ID NO 219
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<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 219

aguauugcac ccgaugagg 19

<210> SEQ ID NO 220
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 220

cucaucgggu gcaauacua 19

<210> SEQ ID NO 221
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<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 221

uaguauugca cccgaugag 19

<210> SEQ ID NO 222
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<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 222

ucaucgggug caauacuag 19

<210> SEQ ID NO 223
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<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 223

cuaguauugc acccgauga 19

<210> SEQ ID NO 224
<211> LENGTH: 19
<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 224

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caucgggugc aauacuagc 19

<210> SEQ ID NO 225
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 225

gcuaguauug cacccgaug 19

<210> SEQ ID NO 226
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<212> TYPE: RNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 226

aucgggugca auacuagcu 19

<210> SEQ ID NO 227
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 227

agcuaguauu gcacccgau 19

<210> SEQ ID NO 228
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 228

ucgggugcaa uacuagcua 19

<210> SEQ ID NO 229
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 229

uagcuaguau ugcacccga 19

<210> SEQ ID NO 230
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 230

auuagcauau aagccuuua 19

<210> SEQ ID NO 231
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 231

uaaaggcuua uaugcuaau 19

<210> SEQ ID NO 232
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 232

uuagcauaua agccuuuau 19

<210> SEQ ID NO 233
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 233

auaaaggcuu auaugcuaa 19

<210> SEQ ID NO 234
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 234

gagcggcgcg gccguguagn n 21

<210> SEQ ID NO 235
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 235

cuacacggcc gcgccgcucn n 21

<210> SEQ ID NO 236
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 236

cguguagcuc ccgggaacun n 21

<210> SEQ ID NO 237
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 237

aguucccggg agcuacacgn n 21

<210> SEQ ID NO 238
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 238

gcugugcuau gugacgaggn n 21

<210> SEQ ID NO 239
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 239

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ccucgucaca uagcacagcn n 21

<210> SEQ ID NO 240
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 240

ugugcuaugu gacgaggccn n 21

<210> SEQ ID NO 241
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 241

ggccucguca cauagcacan n 21

<210> SEQ ID NO 242
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 242

gcagacaagg cauaucuuun n 21

<210> SEQ ID NO 243
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 243

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aaagauaugc cuugucugcn n 21

<210> SEQ ID NO 244
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 244

gaacuacggc auagaguggn n 21

<210> SEQ ID NO 245
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 245

ccacucuaug ccguaguucn n 21

<210> SEQ ID NO 246
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 246

acuacggcau agaguggcan n 21

<210> SEQ ID NO 247
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 247

ugccacucua ugccguagun n 21

<210> SEQ ID NO 248
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 248

ggacuuuagc ccuauuaacn n 21

<210> SEQ ID NO 249
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 249

guuaauaggg cuaaaguccn n 21

<210> SEQ ID NO 250
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 250

gacuuuagcc cuauuaacan n 21

<210> SEQ ID NO 251
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 251

uguuaauagg gcuaaagucn n 21

<210> SEQ ID NO 252
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 252

ccuauuaaca ggauagcuun n 21

<210> SEQ ID NO 253
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 253

aagcuauccu guuaauaggn n 21

<210> SEQ ID NO 254
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 254

uauuaacagg auagcuuaun n 21

<210> SEQ ID NO 255
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)

<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 255

auaagcuauc cuguuaauan n 21

<210> SEQ ID NO 256
<211> LENGTH: 21
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 256

auuaacagga uagcuuaucn n 21

<210> SEQ ID NO 257
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 257

gauaagcuau ccuguuaaun n 21

<210> SEQ ID NO 258
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 258

uuaacaggau agcuuauccn n 21

<210> SEQ ID NO 259
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base

<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 259

ggauaagcua uccuguuaan n 21

<210> SEQ ID NO 260
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 260

aacaggauag cuuauccugn n 21

<210> SEQ ID NO 261
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 261

caggauaagc uauccuguun n 21

<210> SEQ ID NO 262
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 262

caggauagcu uauccugugn n 21

<210> SEQ ID NO 263
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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cacaggauaa gcuauccugn n 21

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agaaugucua cuugaccgun n 21

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acggucaagu agacauucun n 21

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ugucuacuug accgucaccn n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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ggugacgguc aaguagacan n 21

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ucaaguaaag gaguagauan n 21

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uaucuacucc uuuacuugan n 21

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ggcaacaugg cccaaccgun n 21

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Synthetic oligonucleotide
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acgguugggc cauguugccn n 21

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aacauggccc aaccgugggn n 21

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cccacgguug ggccauguun n 21

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cauggcccaa ccgugggcan n 21

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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
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ugcccacggu ugggccaugn n 21

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<400> SEQUENCE: 276

uuguaugguc auggagcgcn n 21

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gcgcuccaug accauacaan n 21

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uguaugguca uggagcgcun n 21

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agcgcuccau gaccauacan n 21

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ucuacagccu uauagguuun n 21

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aaaccuauaa ggcuguagan n 21

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gaagcuagug agcuaggggn n 21

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ccccuagcuc acuagcuucn n 21

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ccucaucggg ugcaauacun n 21

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aguauugcac ccgaugaggn n 21

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cucaucgggu gcaauacuan n 21

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uaguauugca cccgaugagn n 21

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ucaucgggug caauacuagn n 21

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cuaguauugc acccgaugan n 21

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caucgggugc aauacuagcn n 21

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gcuaguauug cacccgaugn n 21

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aucgggugca auacuagcun n 21

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agcuaguauu gcacccgaun n 21

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ucgggugcaa uacuagcuan n 21

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uagcuaguau ugcacccgan n 21

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auuagcauau aagccuuuan n 21

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uaaaggcuua uaugcuaaun n 21

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uuagcauaua agccuuuaun n 21

<210> SEQ ID NO 299
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auaaaggcuu auaugcuaan n 21

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gcuguguuau gugacgaggt t 21

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gccucgucac auaacacagt t 21

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ccggccucgu cacauaacat t 21

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uuaugugacg aggccggact t 21

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<400> SEQUENCE: 313

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<400> SEQUENCE: 314

ugugacgagg ccggacgcgt t 21

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ucgccguugg cuuucgccut t 21

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<400> SEQUENCE: 321

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<400> SEQUENCE: 322

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Synthetic oligonucleotide

<400> SEQUENCE: 323

ucuaugauuc ccagucgcct t 21

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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
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<400> SEQUENCE: 328

gcaguuuacg gguagcaaat t 21

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uuugcuaccc guaaacugct t 21

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caguuuacgg guagcaaagt t 21

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<400> SEQUENCE: 331

cuuugcuacc cguaaacugt t 21

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<400> SEQUENCE: 332

aguuuacggg uagcaaaggt t 21

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<220> FEATURE:
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<400> SEQUENCE: 333

ccuuugcuac ccguaaacut t 21

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<400> SEQUENCE: 334

guuuacgggu agcaaaggut t 21

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<400> SEQUENCE: 335

accuuugcua cccguaaact t 21

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<400> SEQUENCE: 336

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caccuuugcu acccguaaat t 21

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<400> SEQUENCE: 338

aaggugaaag uuuauggcut t 21

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<400> SEQUENCE: 339

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<400> SEQUENCE: 340

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<400> SEQUENCE: 341

uagccauaaa cuuucaccut t 21

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<400> SEQUENCE: 342

ggugaaaguu uauggcuaat t 21

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uuagccauaa acuuucacct t 21

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<400> SEQUENCE: 344

aaguuuaugg cuaaaccugt t 21

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<400> SEQUENCE: 345

cagguuuagc cauaaacuut t 21

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<400> SEQUENCE: 346

guuuauggcu aaaccugagt t 21

<210> SEQ ID NO 347
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cucagguuua gccauaaact t 21

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<400> SEQUENCE: 353

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<400> SEQUENCE: 354

gggcuagccc cuuacaggct t 21

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<400> SEQUENCE: 355

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<210> SEQ ID NO 356
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<400> SEQUENCE: 356

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<400> SEQUENCE: 357

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<210> SEQ ID NO 358
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uuuaagccug uaaggggcut t 21

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<400> SEQUENCE: 360

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<210> SEQ ID NO 361
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<400> SEQUENCE: 361

aguuuaagcc uguaaggggt t 21

<210> SEQ ID NO 362
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<400> SEQUENCE: 362

cuuacaggag cagacuaggt t 21

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aaaagauaug ccuagucugt t 21

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<400> SEQUENCE: 367

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<400> SEQUENCE: 370

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<400> SEQUENCE: 400

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<400> SEQUENCE: 402

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<400> SEQUENCE: 403

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<400> SEQUENCE: 405

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<400> SEQUENCE: 406

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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide

<400> SEQUENCE: 407

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<400> SEQUENCE: 408

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<400> SEQUENCE: 409

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<400> SEQUENCE: 412

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<400> SEQUENCE: 558

uguaugguca uggagcgcut t 21

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<400> SEQUENCE: 559

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<400> SEQUENCE: 560

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aaaccuauaa ggcuguagat t 21

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<400> SEQUENCE: 562

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<400> SEQUENCE: 563

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<400> SEQUENCE: 564

ccucaucggg ugcaauacut t 21

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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide

<400> SEQUENCE: 565

aguauugcac ccgaugaggt t 21

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<400> SEQUENCE: 566

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<400> SEQUENCE: 567

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<400> SEQUENCE: 569

cuaguauugc acccgaugat t 21

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<220> FEATURE:
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<400> SEQUENCE: 570

caucgggugc aauacuagct t 21

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<400> SEQUENCE: 571

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<400> SEQUENCE: 572

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<400> SEQUENCE: 573

agcuaguauu gcacccgaut t 21

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ucgggugcaa uacuagcuat t 21

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aggtcgcgtg tggagcatgt ccagcacgtc tatctgccaa cgcacaccag tcttctcaat 1560

ctgactgtaa tctaatctgt tgtgcttttg ttggacttgg catgtttcca tgaactgcac 1620

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cagacacatt ccttggatgt tgatttttttt tatgatctag taaaggaata ggtaaagtct 1860

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ttgggcattt tggaagctgg tcagctagca ggtttttctgg gatgtcggga gacctagatg 2760

accttatcgg gtgcaatact agctaaggta aagctagaaa cctacactgt cactttactg 2820

agatttctga gtatactttt catattgcct taatgtagca gtaatgtgtt tatgcatttg 2880

tttctttgca cagacatttt gtcaaatatt aaaactctac ttttttatgg cacatattag 2940

catataagcc tttattccaa gaggtattta ttttttcact tgtaaaaaaa taatgtttcc 3000

acgtaaagaa ctctgttata tcctagagga ctctgtcttt tatattcggg ataataaaga 3060

ctttaaagca aaaaaaaaaa aaaaaa 3086

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<211> LENGTH: 2983
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 645

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cctcacggag cccggagtcg acttggagca attgcggtga ggcgacagct ccggcgcaca 180

cccgagaaga agcggcggtg gcggcggccc cagccatgct gtgctatgtg acgaggccgg 240

acgcggtgct gatggaggta gaggtggagg caaaagccaa cggcgaggac tgtctcaacc 300

aggtgtgcag gcgtctaggg atcatcgagg ttgattattt tgggctgcag ttcacgggga 360

gcaaaggtga gagcttatgg ctgaatctga gaaaccggat ctcccagcag atggatgggc 420

tggcacctta ccgccttaaa ctgagggtca agttctttgt ggagcctcat ctcatcttac 480

aggagcagac aaggcatatc tttttcttgc acattaaaga gtccctcttg gcaggccacc 540

tccagtgttc cccagagcag gccgtggaac tcagtgccct cctggctcag accaaatttg 600

gagactacaa ccagaacacc gcccaataca gctatgagga cctgtgtgag aaagagctct 660

ccagctccac tttgaacagc atcgttgcga agcataagga gctggagggc atcagccagg 720

cctctgccga gtaccaggtt ctgcagattg tgtcagcgat ggagaactac ggcatagagt 780

ggcatgctgt gagggacagc gaaggacaga aactcctcat tggggtcgga cctgaaggca 840

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tggccaccca gtcaggaaag aatgtctact tgaccgtcac caaggagtcc ggcaacagca 960

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agcacgtcta cctgcccacc cacaccagtc tcctcaatct gactgtcatc tgatgcgtcc 1560

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aactttgtga agagctattt cactctcaac acccatctgc catgagacat tttcagaaac 1680

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aagaggtatt tatttttca cttgtaaaaa aaataatgtt tcc 2983

<210> SEQ ID NO 646
<211> LENGTH: 1338
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 646

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tattttgggc tgcagttcac ggggagcaaa ggtgagagct tatggctgaa tctgagaaac 180

cggatctccc agcagatgga tgggctggca ccttaccgcc ttaaactgag ggtcaagttc 240

tttgtggagc ctcatctcat cttacaggag cagacaaggc atatcttttt cttgcacatt 300

aaagagtccc tcttggcagg ccacctccag tgttccccag agcaggccgt ggaactcagt 360

gccctcctgg ctcagaccaa atttggagac tacaaccaga acaccgccca atacagctat 420

gaggacctgt gtgagaaaga gctctccagc tccactttga acagcatcgt tgcgaagcat 480

aaggagctgg agggcatcag ccaggcctct gccgagtacc aggttctgca gattgtgtca 540

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ctcattgggg tcggacctga aggcatctcg atctgtaaag aggactttag ccctattaac 660

aggatagctt atcctgtggt gcagatggcc acccagtcag gaaagaatgt ctacttgacc 720

gtcaccaagg agtccggcaa cagcatcgtg ctcctgttta agatgatcag caccagagca 780

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aatctgactg tcatctga 1338

<210> SEQ ID NO 647
<211> LENGTH: 3066
<212> TYPE: DNA
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 647

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caccggagaa gaagcggccg tggcggcggt ggcggcggcc ccagccatgc tgtgctatgt 240

gacgaggccg gacgcggtgc tgatggaggt ggaggtggag gcaaaagcca acggcgagga 300

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gttcacgggt agcaaaggtg aaagcttatg gctgaatctg agaaaccgga tctcccagca 420

gatggatggg ctggcacctt accggcttaa actgagggtc aagttctttg tggagcccca 480

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ggcaggccac ctccagtgtt ccccagagca ggcagtggaa cttagtgccc tcctggccca 600

gaccaaattc ggagactaca accagaacac tgcccaatac agctatgagg acctgtgtga 660

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catcagccag gcttctgcag aataccaagt tctgcagatt gtgtcagcaa tggagaacta 780

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taaagc 3066

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 648

cagccaugcu guguuaugu 19

<210> SEQ ID NO 649
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 649

acauaacaca gcauggcug 19

<210> SEQ ID NO 650
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 650

caggcgacug ggaaucaua 19

<210> SEQ ID NO 651
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 651

uaugauuccc agucgccug 19

<210> SEQ ID NO 652
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 652

gacugggaau cauagaagu 19

<210> SEQ ID NO 653
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 653

acuucuauga uucccaguc 19

<210> SEQ ID NO 654
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 654

acugggaauc auagaaguu 19

<210> SEQ ID NO 655
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 655

aacuucuaug auucccagu 19

<210> SEQ ID NO 656
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 656

gaaucauaga aguugacua 19

<210> SEQ ID NO 657
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 657

uagucaacuu cuaugauuc 19

<210> SEQ ID NO 658
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 658

uaaaccugag aaaccggau 19

<210> SEQ ID NO 659
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 659

auccgguuuc ucagguuua 19

<210> SEQ ID NO 660
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 660

aggcuuaaac uuagaguca 19

<210> SEQ ID NO 661
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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oligonucleotide

<400> SEQUENCE: 661

ugacucuaag uuuaagccu 19

<210> SEQ ID NO 662
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 662

ggcuuaaacu uagagucaa 19

<210> SEQ ID NO 663
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 663

uugacucuaa guuuaagcc 19

<210> SEQ ID NO 664
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 664

acaggagcag acuaggcau 19

<210> SEQ ID NO 665
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 665

augccuaguc ugcuccugu 19

<210> SEQ ID NO 666
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 666

caggagcaga cuaggcaua 19

<210> SEQ ID NO 667
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 667

uaugccuagu cugcuccug 19

<210> SEQ ID NO 668
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 668

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<210> SEQ ID NO 669
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 669

agauaugccu agucugcuc 19

<210> SEQ ID NO 670
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 670

gcagacuagg cauaucuuu 19

<210> SEQ ID NO 671
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 671

aaagauaugc cuagucugc 19

<210> SEQ ID NO 672
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 672

uuggcaggcc accucuugu 19

<210> SEQ ID NO 673
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

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<400> SEQUENCE: 673

acaagaggug gccugccaa 19

<210> SEQ ID NO 674
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 674

uugaacagca uuguugcaa 19

<210> SEQ ID NO 675
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 675

uugcaacaau gcuguucaa 19

<210> SEQ ID NO 676
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 676

cagcugaaua ccaaguuuu 19

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 677

aaaacuuggu auucagcug 19

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<212> TYPE: RNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 678

gucggcaaug gaaaacuau 19

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<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 679

auaguuuucc auugccgac 19

<210> SEQ ID NO 680
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 680

acuauggcau agaauggca 19

<210> SEQ ID NO 681
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 681

ugccauucua ugccauagu 19

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<212> TYPE: RNA
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uucugugcgg gauagcgaa 19

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uucgcuaucc cgcacagaa 19

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<400> SEQUENCE: 684

ggaccugaag gaaucucaa 19

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uugagauucc uucaggucc 19

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<400> SEQUENCE: 686

uaaagaugac uuuagccca 19

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ugggcuaaag ucaucuuua 19

<210> SEQ ID NO 688
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<400> SEQUENCE: 688

aaagaugacu uuagcccaa 19

<210> SEQ ID NO 689
<211> LENGTH: 19
<212> TYPE: RNA
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<400> SEQUENCE: 689

uugggcuaaa gucaucuuu 19

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<212> TYPE: RNA
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<400> SEQUENCE: 690

uagcccaauu aauaggaua 19

<210> SEQ ID NO 691
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<212> TYPE: RNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 691

uauccuauua auugggcua 19

<210> SEQ ID NO 692
<211> LENGTH: 19
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<400> SEQUENCE: 692

ccaauuaaua ggauagcuu 19

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<400> SEQUENCE: 693

aagcuauccu auuaauugg 19

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<400> SEQUENCE: 694

uaauaggaua gcuuauccu 19

<210> SEQ ID NO 695
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<400> SEQUENCE: 695

aggauaagcu auccuauua 19

<210> SEQ ID NO 696
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<400> SEQUENCE: 696

cagcaucgug cucuuguuu 19

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<400> SEQUENCE: 697

aaacaagagc acgaugcug 19

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<400> SEQUENCE: 698

caucgugcuc uuguuuaaa 19

<210> SEQ ID NO 699
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<400> SEQUENCE: 699

uuuaaacaag agcacgaug 19

<210> SEQ ID NO 700
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<400> SEQUENCE: 700

gggcucuacc gagcgauaa 19

<210> SEQ ID NO 701
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<400> SEQUENCE: 701

uuaucgcucg guagagccc 19

<210> SEQ ID NO 702
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 702

gcucuaccga gcgauaaca 19

<210> SEQ ID NO 703
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 703

uguuaucgcu cgguagagc 19

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<210> SEQ ID NO 704
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 704

ucuaccgagc gauaacaga 19

<210> SEQ ID NO 705
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 705

ucuguuaucg cucgguaga 19

<210> SEQ ID NO 706
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 706

uaccgagcga uaacagaga 19

<210> SEQ ID NO 707
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 707

ucucuguuau cgcucggua 19

<210> SEQ ID NO 708
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 708

acagagacgc acgcauucu 19

<210> SEQ ID NO 709
<211> LENGTH: 19
<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 709

agaaugcgug cgucucugu 19

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<220> FEATURE:
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<400> SEQUENCE: 710

gaagggccac uuggcaucu 19

<210> SEQ ID NO 711
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 711

agaugccaag uggcccuuc 19

<210> SEQ ID NO 712
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 712

caucaaagga gguguauga 19

<210> SEQ ID NO 713
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<212> TYPE: RNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 713

ucauacaccu ccuuugaug 19

<210> SEQ ID NO 714
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 714

ggcguugugg accucguuu 19

<210> SEQ ID NO 715
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 715

aaacgagguc cacaacgcc 19

<210> SEQ ID NO 716
<211> LENGTH: 19

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<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 716

guuguggacc ucguuucaa 19

<210> SEQ ID NO 717
<211> LENGTH: 19
<212> TYPE: RNA
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<400> SEQUENCE: 717

uugaaacgag guccacaac 19

<210> SEQ ID NO 718
<211> LENGTH: 19
<212> TYPE: RNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 718

uguggaccuc guuucaaga 19

<210> SEQ ID NO 719
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<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 719

ucuugaaacg agguccaca 19

<210> SEQ ID NO 720
<211> LENGTH: 19
<212> TYPE: RNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 720

cacucgccuc ugaaguccu 19

<210> SEQ ID NO 721
<211> LENGTH: 19
<212> TYPE: RNA
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<400> SEQUENCE: 721

aggacuucag aggcgagug 19

<210> SEQ ID NO 722
<211> LENGTH: 19
<212> TYPE: RNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 722

gcauguccag cacgucuau 19

<210> SEQ ID NO 723
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 723

auagacgugc uggacaugc 19

<210> SEQ ID NO 724
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 724

auguccagca cgucuaucu 19

<210> SEQ ID NO 725
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 725

agauagacgu gcuggacau 19

<210> SEQ ID NO 726
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 726

cucaaucuga cuguaaucu 19

<210> SEQ ID NO 727
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 727

agauuacagu cagauugag 19

<210> SEQ ID NO 728
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 728

caaucugacu guaaucuaa 19

<210> SEQ ID NO 729
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 729

uuagauuaca gucagauug 19

<210> SEQ ID NO 730
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 730

aaucugacug uaaucuaau 19

<210> SEQ ID NO 731
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 731

auuagauuac agucagauu 19

<210> SEQ ID NO 732
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 732

ugcacuauua uaaacuauu 19

<210> SEQ ID NO 733
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 733

aauaguuuau aauagugca 19

<210> SEQ ID NO 734
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 734

auaacacagc uacuccuca 19

<210> SEQ ID NO 735
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 735

ugaggaguag cuguguuau 19

<210> SEQ ID NO 736
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 736

aaacauaucc augcguaga 19

<210> SEQ ID NO 737
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 737

ucuacgcaug gauauguuu 19

<210> SEQ ID NO 738
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 738

aacauaucca ugcguagaa 19

<210> SEQ ID NO 739
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 739

uucuacgcau ggauauguu 19

<210> SEQ ID NO 740
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

oligonucleotide

<400> SEQUENCE: 740

auauccaugc guagaauca 19

<210> SEQ ID NO 741
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 741

ugauucuacg cauggauau 19

<210> SEQ ID NO 742
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 742

uauccaugcg uagaaucaa 19

<210> SEQ ID NO 743
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 743

uugauucuac gcauggaua 19

<210> SEQ ID NO 744
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 744

cguagaauca acaacucca 19

<210> SEQ ID NO 745
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 745

uggaguuguu gauucuacg 19

<210> SEQ ID NO 746
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

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<400> SEQUENCE: 746

cuaguaaagg aauagguaa 19

<210> SEQ ID NO 747
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 747

uuaccuauuc cuuuacuag 19

<210> SEQ ID NO 748
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 748

uaguaaagga auagguaaa 19

<210> SEQ ID NO 749
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 749

uuuaccuauu ccuuuacua 19

<210> SEQ ID NO 750
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 750

aaaggaauag guaaagucu 19

<210> SEQ ID NO 751
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 751

agacuuuacc uauuccuuu 19

<210> SEQ ID NO 752
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 752

aaggaauagg uaaagucuu 19

<210> SEQ ID NO 753
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 753

aagacuuuac cuauuccuu 19

<210> SEQ ID NO 754
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 754

ugaaguggca acauagcca 19

<210> SEQ ID NO 755
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 755

uggcuauguu gccacuuca 19

<210> SEQ ID NO 756
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 756

gaaguggcaa cauagccaa 19

<210> SEQ ID NO 757
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 757

uuggcuaugu ugccacuuc 19

<210> SEQ ID NO 758
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 758

aguuggguac cuuuuagga 19

<210> SEQ ID NO 759
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 759

uccuaaaagg uacccaacu 19

<210> SEQ ID NO 760
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 760

gauguuguaa gucuccuua 19

<210> SEQ ID NO 761
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 761

uaaggagacu uacaacauc 19

<210> SEQ ID NO 762
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 762

guaagucucc uuaauguau 19

<210> SEQ ID NO 763
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 763

auacauuaag gagacuuac 19

<210> SEQ ID NO 764
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 764

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aauguauccu gagguaagu 19

<210> SEQ ID NO 765
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 765

acuuaccuca ggauacauu 19

<210> SEQ ID NO 766
<211> LENGTH: 19
<212> TYPE: RNA
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uccugaggua aguuuccua 19

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uaggaaacuu accucagga 19

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ccuacuggca gcagauuuu 19

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aaaaucugcu gccaguagg 19

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uuuuguaaau uguugucgu 19

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acgacaacaa uuuacaaaa 19

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uguaaauugu ugucguuuu 19

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aaaacgacaa caauuuaca 19

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gauuggaagg caaacaggu 19

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accuguuugc cuuccaauc 19

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aaggcaaaca gguuuacaa 19

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uuguaaaccu guuugccuu 19

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uguugucaga uuuaaacca 19

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ugguuuaaau cugacaaca 19

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aaaccagugu ggcuaguaa 19

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uuacuagcca cacugguuu 19

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augugggugg cucccuauu 19

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aauagggagc cacccacau 19

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ccccacaagc cuuucgauu 19

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<400> SEQUENCE: 785

aaucgaaagg cuugugggg 19

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gccuuucgau uauaaaaua 19

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uauuuuauaa ucgaaaggc 19

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cgauuauaaa auacuacca 19

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ugguaguauu uuauaaucg 19

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<400> SEQUENCE: 790

cuuguuauaa gauuacugu 19

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<400> SEQUENCE: 791

acaguaaucu uauaacaag 19

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<400> SEQUENCE: 792

gauuacugug gaguaguca 19

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<400> SEQUENCE: 793

ugacuacucc acaguaauc 19

<210> SEQ ID NO 794
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<400> SEQUENCE: 794

uacuguggag uagucaagu 19

<210> SEQ ID NO 795
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<212> TYPE: RNA
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<400> SEQUENCE: 795

acuugacuac uccacagua 19

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<400> SEQUENCE: 796

guacaacuga ggguaguua 19

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<212> TYPE: RNA
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<400> SEQUENCE: 797

uaacuacccu caguuguac 19

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<400> SEQUENCE: 798

uacaacugag gguaguuaa 19

<210> SEQ ID NO 799
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<212> TYPE: RNA
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<400> SEQUENCE: 799

uuaacuaccc ucaguugua 19

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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 800

caacugaggg uaguuaacu 19

<210> SEQ ID NO 801
<211> LENGTH: 19
<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 801

aguuaacuac ccucaguug 19

<210> SEQ ID NO 802
<211> LENGTH: 19
<212> TYPE: RNA
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<400> SEQUENCE: 802

acugagggua guuaacuca 19

<210> SEQ ID NO 803
<211> LENGTH: 19
<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 803

ugaguuaacu acccucagu 19

<210> SEQ ID NO 804
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 804

cugaggguag uuaacucau 19

<210> SEQ ID NO 805
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 805

augaguuaac uacccucag 19

<210> SEQ ID NO 806
<211> LENGTH: 19
<212> TYPE: RNA
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<400> SEQUENCE: 806

gaggguaguu aacucauca 19

<210> SEQ ID NO 807
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<220> FEATURE:
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<400> SEQUENCE: 807

ugaugaguua acuacccuc 19

<210> SEQ ID NO 808
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 808

ggguaguuaa cucaucacu 19

<210> SEQ ID NO 809
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<400> SEQUENCE: 809

agugaugagu uaacuaccc 19

<210> SEQ ID NO 810
<211> LENGTH: 19
<212> TYPE: RNA
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<400> SEQUENCE: 810

gguaguuaac ucaucacuu 19

<210> SEQ ID NO 811
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 811

aagugaugag uuaacuacc 19

<210> SEQ ID NO 812
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 812

uaguuaacuc aucacuucu 19

<210> SEQ ID NO 813
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 813

agaagugaug aguuaacua 19

<210> SEQ ID NO 814
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 814

ugguguugcu uugcuugaa 19

<210> SEQ ID NO 815
<211> LENGTH: 19
<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 815

uucaagcaaa gcaacacca 19

<210> SEQ ID NO 816
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 816

auagccuuac cauaaguau 19

<210> SEQ ID NO 817
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 817

auacuuaugg uaaggcuau 19

<210> SEQ ID NO 818
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 818

uaccauaagu auuuagaua 19

<210> SEQ ID NO 819
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

oligonucleotide

<400> SEQUENCE: 819

uaucuaaaua cuuauggua 19

<210> SEQ ID NO 820
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 820

aaguaagugc uuaaguauu 19

<210> SEQ ID NO 821
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 821

aauacuuaag cacuuacuu 19

<210> SEQ ID NO 822
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 822

aguauuaacu uuggguugu 19

<210> SEQ ID NO 823
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 823

acaacccaaa guuaauacu 19

<210> SEQ ID NO 824
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 824

guauguuucg aagggguuu 19

<210> SEQ ID NO 825
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

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<400> SEQUENCE: 825

aaaccccuuc gaaacauac 19

<210> SEQ ID NO 826
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 826

cuggucagcu agcagguuu 19

<210> SEQ ID NO 827
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 827

aaaccugcua gcugaccag 19

<210> SEQ ID NO 828
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 828

uggucagcua gcagguuuu 19

<210> SEQ ID NO 829
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 829

aaaaccugcu agcugacca 19

<210> SEQ ID NO 830
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 830

gucagcuagc agguuuucu 19

<210> SEQ ID NO 831
<211> LENGTH: 19
<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 831

agaaaaccug cuagcugac 19

<210> SEQ ID NO 832
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 832

ggaugucggg agaccuaga 19

<210> SEQ ID NO 833
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 833

ucuaggucuc ccgacaucc 19

<210> SEQ ID NO 834
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 834

gaugucggga gaccuagau 19

<210> SEQ ID NO 835
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 835

aucuaggucu cccgacauc 19

<210> SEQ ID NO 836
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 836

ugucgggaga ccuagauga 19

<210> SEQ ID NO 837
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 837

ucaucuaggu cucccgaca 19

<210> SEQ ID NO 838
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 838

cgggugcaau acuagcuaa 19

<210> SEQ ID NO 839
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 839

uuagcuagua uugcacccg 19

<210> SEQ ID NO 840
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 840

gugcaauacu agcuaaggu 19

<210> SEQ ID NO 841
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 841

accuuagcua guauugcac 19

<210> SEQ ID NO 842
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 842

ugcaauacua gcuaaggua 19

<210> SEQ ID NO 843
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 843

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uaccuuagcu aguauugca 19

<210> SEQ ID NO 844
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 844

gcaauacuag cuaagguaa 19

<210> SEQ ID NO 845
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 845

uuaccuuagc uaguauugc 19

<210> SEQ ID NO 846
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 846

uacuagcuaa gguaaagcu 19

<210> SEQ ID NO 847
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 847

agcuuuaccu uagcuagua 19

<210> SEQ ID NO 848
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 848

acuagcuaag guaaagcua 19

<210> SEQ ID NO 849
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 849

uagcuuuacc uuagcuagu 19

<210> SEQ ID NO 850
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 850

uagcuaaggu aaagcuaga 19

<210> SEQ ID NO 851
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 851

ucuagcuuua ccuuagcua 19

<210> SEQ ID NO 852
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 852

aauguagcag uaauguguu 19

<210> SEQ ID NO 853
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 853

aacacauuac ugcuacauu 19

<210> SEQ ID NO 854
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 854

ggcacauauu agcauauaa 19

<210> SEQ ID NO 855
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 855

uuauaugcua auaugugcc 19

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<400> SEQUENCE: 856

aaauaauguu uccacguaa 19

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<400> SEQUENCE: 857

uuacguggaa acauuauuu 19

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<400> SEQUENCE: 858

uaauguuucc acguaaaga 19

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<400> SEQUENCE: 859

ucuuuacgug gaaacauua 19

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<400> SEQUENCE: 860

aauguuucca cguaaagaa 19

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uucuuuacgu ggaaacauu 19

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<400> SEQUENCE: 862

aagaacucug uuauauccu 19

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aggauauaac agaguucuu 19

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<400> SEQUENCE: 864

agaacucugu uauauccua 19

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<400> SEQUENCE: 865

uaggauauaa cagaguucu 19

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<400> SEQUENCE: 866

ugucuuuuau auucgggau 19

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<400> SEQUENCE: 867

aucccgaaua uaaaagaca 19

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<211> LENGTH: 19
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<400> SEQUENCE: 868

gucuuuuaua uucgggaua 19

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<400> SEQUENCE: 869

uaucccgaau auaaaagac 19

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<400> SEQUENCE: 870

ucuuuuauau ucgggauaa 19

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uuaucccgaa uauaaaaga 19

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cuuuuauauu cgggauaau 19

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<400> SEQUENCE: 873

auuaucccga auauaaaag 19

<210> SEQ ID NO 874
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<400> SEQUENCE: 874

ggauaauaaa gacuuuaaa 19

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uuuaaagucu uuauuaucc 19

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 876

cagccaugcu guguuaugun n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 877

acauaacaca gcauggcugn n 21

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<400> SEQUENCE: 878

caggcgacug ggaaucauan n 21

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uaugauuccc agucgccugn n 21

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<400> SEQUENCE: 880

gacugggaau cauagaagun n 21

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<400> SEQUENCE: 881

acuucuauga uucccagucn n 21

<210> SEQ ID NO 882
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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<400> SEQUENCE: 882

acugggaauc auagaaguun n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 883

aacuucuaug auucccagun n 21

<210> SEQ ID NO 884
<211> LENGTH: 21
<212> TYPE: DNA
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<221> NAME/KEY: modified_base
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 884

gaaucauaga aguugacuan n 21

<210> SEQ ID NO 885
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<212> TYPE: DNA
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<220> FEATURE:
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 885

uagucaacuu cuaugauucn n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 886

uaaaccugag aaaccggaun n 21

<210> SEQ ID NO 887
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 887

auccgguuuc ucagguuuan n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 888

aggcuuaaac uuagagucan n 21

<210> SEQ ID NO 889
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 889

ugacucuaag uuuaagccun n 21

<210> SEQ ID NO 890
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 890

ggcuuaaacu uagagucaan n 21

<210> SEQ ID NO 891
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 891

uugacucuaa guuuaagccn n 21

<210> SEQ ID NO 892
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 892

acaggagcag acuaggcaun n 21

<210> SEQ ID NO 893
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 893

augccuaguc ugcuccugun n 21

<210> SEQ ID NO 894
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 894

caggagcaga cuaggcauan n 21

<210> SEQ ID NO 895
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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uaugccuagu cugcuccugn n 21

<210> SEQ ID NO 896
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 896

gagcagacua ggcauaucun n 21

<210> SEQ ID NO 897
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 897

agauaugccu agucugcucn n 21

<210> SEQ ID NO 898
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 898

gcagacuagg cauaucuuun n 21

<210> SEQ ID NO 899
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 899

aaagauaugc cuagucugcn n 21

<210> SEQ ID NO 900
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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uuggcaggcc accucuugun n 21

<210> SEQ ID NO 901
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<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 901

acaagaggug gccugccaan n 21

<210> SEQ ID NO 902
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:

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Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 902

uugaacagca uuguugcaan n 21

<210> SEQ ID NO 903
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 903

uugcaacaau gcuguucaan n 21

<210> SEQ ID NO 904
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 904

cagcugaaua ccaaguuuun n 21

<210> SEQ ID NO 905
<211> LENGTH: 21
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 905

aaaacuuggu auucagcugn n 21

<210> SEQ ID NO 906
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 906

gucggcaaug gaaaacuaun n 21

<210> SEQ ID NO 907
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 907

auaguuuucc auugccgacn n 21

<210> SEQ ID NO 908
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<212> TYPE: DNA
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<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 908

acuauggcau agaauggcan n 21

<210> SEQ ID NO 909
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 909

ugccauucua ugccauagun n 21

<210> SEQ ID NO 910
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
Synthetic oligonucleotide
<220> FEATURE:
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 910

uucugugcgg gauagcgaan n 21

<210> SEQ ID NO 911
<211> LENGTH: 21
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide
<220> FEATURE:
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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uucgcuaucc cgcacagaan n 21

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oligonucleotide
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Synthetic oligonucleotide
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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ggaccugaag gaaucucaan n 21

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oligonucleotide
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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uugagauucc uucagguccn n 21

<210> SEQ ID NO 914
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oligonucleotide
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 914

uaaagaugac uuuagcccan n 21

<210> SEQ ID NO 915
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 915

ugggcuaaag ucaucuuuan n 21

<210> SEQ ID NO 916
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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aaagaugacu uuagcccaan n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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uugggcuaaa gucaucuuun n 21

<210> SEQ ID NO 918
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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uagcccaauu aauaggauan n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 919

uauccuauua auugggcuan n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 920

ccaauuaaua ggauagcuun n 21

<210> SEQ ID NO 921
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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aagcuauccu auuaauuggn n 21

<210> SEQ ID NO 922
<211> LENGTH: 21
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 922

uaauaggaua gcuuauccun n 21

<210> SEQ ID NO 923
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 923

aggauaagcu auccuauuan n 21

<210> SEQ ID NO 924
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 924

cagcaucgug cucuuguuun n 21

<210> SEQ ID NO 925
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
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<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 925

aaacaagagc acgaugcugn n 21

<210> SEQ ID NO 926
<211> LENGTH: 21
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 926

caucgugcuc uuguuuaaan n 21

<210> SEQ ID NO 927
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 927

uuuaaacaag agcacgaugn n 21

<210> SEQ ID NO 928
<211> LENGTH: 21
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<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 928

gggcucuacc gagcgauaan n 21

<210> SEQ ID NO 929
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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uuaucgcucg guagagcccn n 21

<210> SEQ ID NO 930
<211> LENGTH: 21

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<212> TYPE: DNA
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<220> FEATURE:
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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gcucuaccga gcgauaacan n 21

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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 931

uguuaucgcu cgguagagcn n 21

<210> SEQ ID NO 932
<211> LENGTH: 21
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 932

ucuaccgagc gauaacagan n 21

<210> SEQ ID NO 933
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 933

ucuguuaucg cucgguagan n 21

<210> SEQ ID NO 934

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<211> LENGTH: 21
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 934

uaccgagcga uaacagagan n 21

<210> SEQ ID NO 935
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 935

ucucuguuau cgcucgguan n 21

<210> SEQ ID NO 936
<211> LENGTH: 21
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 936

acagagacgc acgcauucun n 21

<210> SEQ ID NO 937
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<220> FEATURE:
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 937

agaaugcgug cgucucugun n 21

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<210> SEQ ID NO 938
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 938

gaagggccac uuggcaucun n 21

<210> SEQ ID NO 939
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 939

agaugccaag uggcccuucn n 21

<210> SEQ ID NO 940
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 940

caucaaagga gguguaugan n 21

<210> SEQ ID NO 941
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 941

ucauacaccu ccuuugaugn n 21

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<210> SEQ ID NO 942
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 942

ggcguugugg accucguuun n 21

<210> SEQ ID NO 943
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 943

aaacgagguc cacaacgccn n 21

<210> SEQ ID NO 944
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 944

guuguggacc ucguuucaan n 21

<210> SEQ ID NO 945
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 945

uugaaacgag guccacaacn n 21

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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 946

uguggaccuc guuucaagan n 21

<210> SEQ ID NO 947
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 947

ucuugaaacg agguccacan n 21

<210> SEQ ID NO 948
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
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<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 948

cacucgccuc ugaaguccun n 21

<210> SEQ ID NO 949
<211> LENGTH: 21
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 949

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aggacuucag aggcgagugn n 21

<210> SEQ ID NO 950
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 950

gcauguccag cacgucuaun n 21

<210> SEQ ID NO 951
<211> LENGTH: 21
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 951

auagacgugc uggacaugcn n 21

<210> SEQ ID NO 952
<211> LENGTH: 21
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 952

auguccagca cgucuaucun n 21

<210> SEQ ID NO 953
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 953

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agauagacgu gcuggacaun n 21

<210> SEQ ID NO 954
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 954

cucaaucuga cuguaaucun n 21

<210> SEQ ID NO 955
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 955

agauuacagu cagauugagn n 21

<210> SEQ ID NO 956
<211> LENGTH: 21
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 956

caaucugacu guaaucuaan n 21

<210> SEQ ID NO 957
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uuagauuaca gucagauugn n 21

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aaucugacug uaaucuaaun n 21

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auuagauuac agucagauun n 21

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ugcacuauua uaaacuauun n 21

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aauaguuuau aauagugcan n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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auaacacagc uacuccucan n 21

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<400> SEQUENCE: 963

ugaggaguag cuguguuaun n 21

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<400> SEQUENCE: 964

aaacauaucc augcguagan n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 965

ucuacgcaug gauauguuun n 21

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<400> SEQUENCE: 966

aacauaucca ugcguagaan n 21

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<400> SEQUENCE: 967

uucuacgcau ggauauguun n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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auauccaugc guagaaucan n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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ugauucuacg cauggauaun n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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uauccaugcg uagaaucaan n 21

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uugauucuac gcauggauan n 21

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<400> SEQUENCE: 972

cguagaauca acaacuccan n 21

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<221> NAME/KEY: modified_base
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 973

uggaguuguu gauucuacgn n 21

<210> SEQ ID NO 974
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 974

cuaguaaagg aauagguaan n 21

<210> SEQ ID NO 975
<211> LENGTH: 21
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 975

uuaccuauuc cuuuacuagn n 21

<210> SEQ ID NO 976
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 976

uaguaaagga auagguaaan n 21

<210> SEQ ID NO 977
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<220> FEATURE:
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 977

uuuaccuauu ccuuuacuan n 21

<210> SEQ ID NO 978
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 978

aaaggaauag guaaagucun n 21

<210> SEQ ID NO 979
<211> LENGTH: 21
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 979

agacuuuacc uauuccuuun n 21

<210> SEQ ID NO 980
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 980

aaggaauagg uaaagucuun n 21

<210> SEQ ID NO 981
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Synthetic oligonucleotide
<220> FEATURE:
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 981

aagacuuuac cuauuccuun n 21

<210> SEQ ID NO 982
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 982

ugaaguggca acauagccan n 21

<210> SEQ ID NO 983
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 983

uggcuauguu gccacuucan n 21

<210> SEQ ID NO 984
<211> LENGTH: 21
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 984

gaaguggcaa cauagccaan n 21

<210> SEQ ID NO 985
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<212> TYPE: DNA
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<220> FEATURE:

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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
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<220> FEATURE:
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 985

uuggcuaugu ugccacuucn n 21

<210> SEQ ID NO 986
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
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<220> FEATURE:
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 986

aguuggguac cuuuuaggan n 21

<210> SEQ ID NO 987
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 987

uccuaaaagg uacccaacun n 21

<210> SEQ ID NO 988
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<220> FEATURE:
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 988

gauguuguaa gucuccuuan n 21

<210> SEQ ID NO 989
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 989

uaaggagacu uacaacaucn n 21

<210> SEQ ID NO 990
<211> LENGTH: 21
<212> TYPE: DNA
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 990

guaagucucc uuaauguaun n 21

<210> SEQ ID NO 991
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<220> FEATURE:
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 991

auacauuaag gagacuuacn n 21

<210> SEQ ID NO 992
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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aauguauccu gagguaagun n 21

<210> SEQ ID NO 993
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 993

acuuaccuca ggauacauun n 21

<210> SEQ ID NO 994
<211> LENGTH: 21
<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 994

uccugaggua aguuuccuan n 21

<210> SEQ ID NO 995
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 995

uaggaaacuu accucaggan n 21

<210> SEQ ID NO 996
<211> LENGTH: 21
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<220> FEATURE:
<221> NAME/KEY: modified_base
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 996

ccuacuggca gcagauuuun n 21

<210> SEQ ID NO 997
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<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 997

aaaaucugcu gccaguaggn n 21

<210> SEQ ID NO 998
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 998

uuuuguaaau uguugucgun n 21

<210> SEQ ID NO 999
<211> LENGTH: 21
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 999

acgacaacaa uuuacaaaan n 21

<210> SEQ ID NO 1000
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1000

uguaaauugu ugucguuuun n 21

<210> SEQ ID NO 1001
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1001

aaaacgacaa caauuuacan n 21

<210> SEQ ID NO 1002
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
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gauuggaagg caaacaggun n 21

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aaggcaaaca gguuuacaan n 21

<210> SEQ ID NO 1005
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uguugucaga uuuaaaccan n 21

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ugguuuaaau cugacaacan n 21

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aaaccagugu ggcuaguaan n 21

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uuacuagcca cacugguuun n 21

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ccccacaagc cuuucgauun n 21

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aaucgaaagg cuuguggggn n 21

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<400> SEQUENCE: 1014

gccuuucgau uauaaaauan n 21

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uauuuuauaa ucgaaaggcn n 21

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cgauuauaaa auacuaccan n 21

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ugguaguauu uuauaaucgn n 21

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cuuguuauaa gauuacugun n 21

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acaguaaucu uauaacaagn n 21

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gauuacugug gaguagucan n 21

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ugacuacucc acaguaaucn n 21

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uacuguggag uagucaagun n 21

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acuugacuac uccacaguan n 21

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guacaacuga ggguaguuan n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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uaacuacccu caguuguacn n 21

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uacaacugag gguaguuaan n 21

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uuaacuaccc ucaguuguan n 21

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caacugaggg uaguuaacun n 21

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aguuaacuac ccucaguugn n 21

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acugagggua guuaacucan n 21

<210> SEQ ID NO 1031
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ugaguuaacu acccucagun n 21

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cugaggguag uuaacucaun n 21

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augaguuaac uacccucagn n 21

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gaggguaguu aacucaucan n 21

<210> SEQ ID NO 1035
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ugaugaguua acuacccucn n 21

<210> SEQ ID NO 1036
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ggguaguuaa cucaucacun n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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agugaugagu uaacuacccn n 21

<210> SEQ ID NO 1038
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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gguaguuaac ucaucacuun n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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aagugaugag uuaacuaccn n 21

<210> SEQ ID NO 1040
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<400> SEQUENCE: 1040

uaguuaacuc aucacuucun n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

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agaagugaug aguuaacuan n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1042

ugguguugcu uugcuugaan n 21

<210> SEQ ID NO 1043
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<221> NAME/KEY: modified_base
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1043

uucaagcaaa gcaacaccan n 21

<210> SEQ ID NO 1044
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<221> NAME/KEY: modified_base
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1044

auagccuuac cauaaguaun n 21

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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1045

auacuuaugg uaaggcuaun n 21

<210> SEQ ID NO 1046
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1046

uaccauaagu auuuagauan n 21

<210> SEQ ID NO 1047
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<400> SEQUENCE: 1047

uaucuaaaua cuuaugguan n 21

<210> SEQ ID NO 1048
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<220> FEATURE:
<221> NAME/KEY: modified_base

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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1048

aaguaagugc uuaaguauun n 21

<210> SEQ ID NO 1049
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1049

aauacuuaag cacuuacuun n 21

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1050

aguauuaacu uuggguugun n 21

<210> SEQ ID NO 1051
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<220> FEATURE:
<221> NAME/KEY: modified_base
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<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1051

acaacccaaa guuaauacun n 21

<210> SEQ ID NO 1052
<211> LENGTH: 21
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:

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<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1052

guauguuucg aaggguuun n 21

<210> SEQ ID NO 1053
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1053

aaaccccuuc gaaacauacn n 21

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<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1054

cuggucagcu agcagguuun n 21

<210> SEQ ID NO 1055
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1055

aaaccugcua gcugaccagn n 21

<210> SEQ ID NO 1056
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide

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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1056

uggucagcua gcagguuuun n 21

<210> SEQ ID NO 1057
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1057

aaaaccugcu agcugaccan n 21

<210> SEQ ID NO 1058
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1058

gucagcuagc agguuuucun n 21

<210> SEQ ID NO 1059
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1059

agaaaaccug cuagcugacn n 21

<210> SEQ ID NO 1060
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:

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Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1060

ggaugucggg agaccuagan n 21

<210> SEQ ID NO 1061
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1061

ucuaggucuc ccgacauccn n 21

<210> SEQ ID NO 1062
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1062

gaugucggga gaccuagaun n 21

<210> SEQ ID NO 1063
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1063

aucuaggucu cccgacaucn n 21

<210> SEQ ID NO 1064
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1064

ugucgggaga ccuagaugan n 21

<210> SEQ ID NO 1065
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1065

ucaucuaggu cucccgacan n 21

<210> SEQ ID NO 1066
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1066

cgggugcaau acuagcuaan n 21

<210> SEQ ID NO 1067
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1067

uuagcuagua uugcacccgn n 21

<210> SEQ ID NO 1068
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1068

gugcaauacu agcuaaggun n 21

<210> SEQ ID NO 1069
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1069

accuuagcua guauugcacn n 21

<210> SEQ ID NO 1070
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1070

ugcaauacua gcuaagguan n 21

<210> SEQ ID NO 1071
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1071

uaccuuagcu aguauugcan n 21

<210> SEQ ID NO 1072
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1072

gcaauacuag cuaagguaan n 21

<210> SEQ ID NO 1073
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1073

uuaccuuagc uaguauugcn n 21

<210> SEQ ID NO 1074
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1074

uacuagcuaa gguaaagcun n 21

<210> SEQ ID NO 1075
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1075

agcuuuaccu uagcuaguan n 21

<210> SEQ ID NO 1076
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1076

acuagcuaag guaaagcuan n 21

<210> SEQ ID NO 1077
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1077

uagcuuuacc uuagcuagun n 21

<210> SEQ ID NO 1078
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1078

uagcuaaggu aaagcuagan n 21

<210> SEQ ID NO 1079
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
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<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1079

ucuagcuuua ccuuagcuan n 21

<210> SEQ ID NO 1080
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1080

aauguagcag uaauguguun n 21

<210> SEQ ID NO 1081
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1081

aacacauuac ugcuacauun n 21

<210> SEQ ID NO 1082
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1082

ggcacauauu agcauauaan n 21

<210> SEQ ID NO 1083
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1083

uuauaugcua auaugugccn n 21

<210> SEQ ID NO 1084
<211> LENGTH: 21
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1084

aaauaauguu uccacguaan n 21

<210> SEQ ID NO 1085
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1085

uuacguggaa acauuauuun n 21

<210> SEQ ID NO 1086
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1086

uaauguuucc acguaaagan n 21

<210> SEQ ID NO 1087
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1087

ucuuuacgug gaaacauuan n 21

<210> SEQ ID NO 1088
<211> LENGTH: 21

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1088

aauguuucca cguaaagaan n 21

<210> SEQ ID NO 1089
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1089

uucuuuacgu ggaaacauun n 21

<210> SEQ ID NO 1090
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1090

aagaacucug uuauauccun n 21

<210> SEQ ID NO 1091
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1091

aggauauaac agaguucuun n 21

<210> SEQ ID NO 1092

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<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1092

agaacucugu uauauccuan n 21

<210> SEQ ID NO 1093
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: a, c, t, g, u, unknown or other

<400> SEQUENCE: 1093

uaggauauaa cagaguucun n 21

<210> SEQ ID NO 1094
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ugucuuuuau auucgggaun n 21

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ucuuuuauau ucgggauaan n 21

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auuaucccga auauaaaagn n 21

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ggauaauaaa gacuuuaaan n 21

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uuuaaagucu uuauuauccn n 21

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1 5 10 15

Leu Glu Ala Leu Ala Glu Ala Ala Ala Ala Gly Gly Cys
20 25

<210> SEQ ID NO 1105
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<400> SEQUENCE: 1105

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Glu Ala Leu Ala Glu Ala Leu Ala Ala Ala Ala Gly Gly Cys
20 25 30

<210> SEQ ID NO 1106
<211> LENGTH: 15
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<400> SEQUENCE: 1106

Ala Leu Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Glu Ala
1 5 10 15

<210> SEQ ID NO 1107
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1107

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agccgcccat cccgcagggc cggtctgcca gcgagacgag agttggcgag ggcggaggag 180

tgccgggaat cccgccacac cggctatagc caggcccccа gcgcgggcct tggagagcgc 240

gtgaaggcgg gcatcccctt gacccggccg accatccccg tgcccctgcg tccctgcgct 300

ccaacgtccg cgcggccacc atgatgcaaa tctgcgacac ctacaaccag aagcactcgc 360

tctttaacgc catgaatcgc ttcattggcg ccgtgaacaa catggaccag acggtgatgg 420

tgcccagctt gctgcgcgac gtgcccctgg ctgaccccgg gttagacaac gatgttggcg 480

tggaggtagg cggcagtggc ggctgcctgg aggagcgcac gcccccagtc cccgactcgg 540

gaagcgccaa tggcagcttt ttcgcgccct ctcgggacat gtacagccac tacgtgcttc 600

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ggagcgagga gggcagtgcc tggaagtcca aggacatcct ggtggacctg ggccacttgg	720
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aagcaaatgt gtcaactaaa ttggacaagc gtctggtcct cattaatctg ccaatgaatg	1860
gtttcgtcat taaataaaaa tcaatttaat tgatttacta gcaaaaaaaa aaaaaa	1916

The invention claimed is:

1. A double-stranded ribonucleic acid (dsRNA) for inhibiting expression of Mylip/Idol, wherein said dsRNA comprises a sense strand and an antisense strand, the antisense strand comprising a region of complementarity to a Mylip/Idol transcript which comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of SEQ ID NO: 21.

2. The dsRNA of claim **1**, wherein said dsRNA comprises at least one modified nucleotide.

3. The dsRNA of claim **2**, wherein at least one of said modified nucleotides is chosen from the group consisting of:

a 2'-O-methyl modified nucleotide; a nucleotide comprising a 5'-phosphorothioate group; a terminal nucleotide linked to a cholesteryl derivative or dodecanoic acid bisdecylamide group; a 2'-deoxy-2'-fluoro modified nucleotide; a 2'-deoxy-modified nucleotide; a locked nucleotide; an abasic nucleotide; 2'-amino-modified nucleotide; 2'-alkyl-modified nucleotide; morpholino nucleotide; a phosphoramidate; and a non-natural base comprising nucleotide.

4. The dsRNA of claim **1**, wherein the region of complementarity is at least 17 nucleotides in length.

5. The dsRNA of claim **1**, wherein the region of complementarity is between 19 and 21 nucleotides in length.

6. The dsRNA of claim **5**, wherein the region of complementarity is 19 nucleotides in length.

7. The dsRNA of claim **1**, wherein each strand is no more than 30 nucleotides in length.

8. The dsRNA of claim **1**, wherein at least one strand comprises a 3' overhang of at least 1 nucleotide.

9. The dsRNA of claim **1**, further comprising a ligand.

10. The dsRNA of claim **9**, wherein the ligand is conjugated to the 3' end of the sense strand of the dsRNA.

11. A dsRNA for inhibiting the expression of Mylip/Idol, wherein the dsRNA comprises a sense strand consisting of a nucleotide sequence selected from the group consisting of:

SEQ ID NOs: 20, 22, 24, 26, 28, 32, and 34 and an antisense strand consisting of a nucleotide sequence selected from the group consisting of:

SEQ ID NOs: 21, 23, 25, 27, 29, 33, and 35.

12. A pharmaceutical composition for inhibiting expression of a Mylip/Idol gene comprising a dsRNA comprising a sense strand and an antisense strand, the antisense strand comprising a region of complementarity to a Mylip/Idol transcript which comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the sequence of SEQ ID NO: 21.

13. The pharmaceutical composition of claim **12**, further comprising a lipid formulation.

14. The pharmaceutical composition of claim **13**, wherein the lipid formulation is a SNALP, or XTC formulation.

15. A method of treating a disorder mediated by Mylip/Idol expression comprising administering to a human in need of such treatment a therapeutically effective amount of a dsRNA comprising a sense strand and an antisense strand,

the antisense strand comprising a region of complementarity to a Mylip/Idol transcript which comprises at least

15 contiguous nucleotides differing by no more than 3 nucleotides from the sequence of SEQ ID NO: 21;

or a pharmaceutical composition comprising a dsRNA comprising a sense strand and an antisense strand,

the antisense strand comprising a region of complementarity to a Mylip/Idol transcript which comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from one of the sequence of SEQ ID NO: 21.

16. The method of claim **15**, wherein the human has a lipid disorder.

17. The method of claim **15**, wherein the human has a disorder associated with cholesterol metabolism.

18. The method of claim **15**, wherein the human has diabetes or atherosclerosis.

19. The method of claim **17**, wherein the administration of the dsRNA to the subject causes a decrease in Low Density Lipoprotein cholesterol (LDLc) in the serum of the subject by at least 10%.

20. The method of claim **15**, wherein the dsRNA is administered at a concentration of 0.01 mg/kg-5 mg/kg bodyweight of the subject.

21. The dsRNA of claim **1**, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of SEQ ID NO: 20 and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the corresponding antisense nucleotide sequence of SEQ ID NO: 21.

22. The method of claim **15**, wherein said dsRNA comprises at least one modified nucleotide.

23. The method of claim **22**, wherein at least one of said modified nucleotides is chosen from the group consisting of: a 2'-methyl modified nucleotide; a nucleotide comprising a 5'-phosphorothioate group; a terminal nucleotide linked to a cholesteryl derivative or dodecanoic acid bisdecylamide group; a 2'-deoxy-2'-fluoro modified nucleotide; a 2'-deoxy-modified nucleotide; a locked nucleotide; an abasic nucleotide; 2'-amino-modified nucleotide; 2'-alkyl-modified nucleotide; morpholino nucleotide; a phosphoramidate; and a non-natural base comprising nucleotide.

24. The method of claim **15**, wherein the region of complementarity is at least 17 nucleotides in length.

25. The method of claim **15**, wherein the region of complementarity is between 19 and 21 nucleotides in length.

26. The method of claim **15**, wherein the region of complementarity is 19 nucleotides in length.

27. The method of claim **15**, wherein each strand is no more than 30 nucleotides in length.

28. The method of claim **15**, wherein at least one strand comprises a 3' overhang of at least 1 nucleotide.

29. The method of claim **15**, wherein the dsRNA further comprises a ligand.

30. The method of claim **29**, wherein the ligand is conjugated to the 3' end of the sense strand of the dsRNA.

31. A method of treating a disorder mediated by Mylip/Idol expression comprising administering to a human in need of such treatment a therapeutically effective amount of a dsRNA comprising a sense strand consisting of a nucleotide sequence selected from the group consisting of:

SEQ ID NOs: 20, 22, 24, 26, 28, 32, and 34 and an antisense strand consisting of a nucleotide sequence selected from the group consisting of:

SEQ ID NOs: 21, 23, 25, 27, 29, 33, and 35.

* * * * *